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us-09-455-978b-2.rag

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 10, 2004, 15:18:30 ; Search time 84.6574 Seconds (without alignments) 1632.058 Million cell updates/sec Run on:

US-09-455-978B-2 Title: Perfect score:

1 MSNDNDTLVTADVRNGIDGH........ATDQQVRTVEEVRETVGKLS 489 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* 1: geneseqp19Rnc.* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* ٠. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Ω.	Aae04641 Halobacte		Abu38469 Protein e	Aab96493 Putative	Abu38250 Protein e		Aab96709 Putative	Abu41746 Protein e	Ada33885 Acinetoba	Abu40238 Protein e	Abu49667 Protein e	Aab26596 Synechocy	Aab96382 Putative	Abu23101 Protein e	Abu49142 Protein e	Abm68096 Photorhab	Abb49909 Listeria	Abu24381 Protein e	Abm68095 Photorhab	Abu49354 Protein e	Abu49678 Protein e	Abu41640 Protein e	Abu49123 Protein e	Abu48593 Protein e	Aab14148 Bordetell
SUMMARIES	αI	AAE04641	AAE04642	ABU38469	AAB96493	ABU38250	AAB96483	AAB96709	ABU41746	ADA33885	ABU40238	ABU49667	AAB26596	AAB96382	ABU23101	ABU49142	ABM68096	ABB49909	ABU24381	ABM68095	ABU49354	ABU49678	ABU41640	ABU49123	ABU48593	AAB14148
	DB	4	4	9	4	9	4	4	9	9	9	و	m	4	9	9	9	Ŋ	9	9	9	9	9	9	9	3
	& Query Match Length	489	432	535	739	682	435	501	680	709	989	644	891	374	539	626	265	601	989	545	641	643	501	541	845	511
ن	Query Match	100.0	17.2	16.7	16.2	16.1	15.9	15.7	15.6	15.6	15.5	15.1	15.0	14.9	14.9	14.5	14.5	14.2		13.6	13.6	13.2	13.1	13.1	12.9	12.4
	Score	2394	412.5	399.5	387.5	386.5	380	375	374.5	373.5	371.5	361	359.5	356.5	356.5	348	346.5	339.5	338	326	326	315	314.5	313.5	308	298
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ABG24223	AAW98798	AAW71554	AAB46327	AAW98797	AAW71553	AAB46345	AAY10961	ABU51211	AAW20287	AAW20769	AAY19897	AAY19896	ABU19306	AAY19800	AA Y19799	AAB52596	ABU50773	AAW05196	ABB49349	
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297.5	289	289	289	284	284	284	280	277.5	276	273.5	269	269	269	266	266	257	257	254	253	
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Halobacterium salinarium HemAT-Hs protein. AAE04641 standard; protein; 489 AA. (revised)
(first entry) 11-SEP-2003 04-SEP-2001 AAE04641; RESULT 1

Haem binding protein, HemAT-Hs, HemAT-Bs, gaseous ligand sensor, oxygen storage, artificial photosynthesis, signalling function, alpha-haemoglobin, myoglobin, therapy.

Halobacterium salinarum.

WO200140475-A2.

07-JUN-2001.

05-DEC-2000; 2000WO-US033048.

99US-00455978. 06-DEC-1999;

(UYHA-) UNIV HAWAII.

Alam M, Larsen R;

WPI; 2001-374832/39. N-PSDB; AAD08991 Novel isolated bacterial heme binding protein, HemAT-Hs or HemAT-Bs which reversibly binds oxygen with low affinity, useful for controlled storage of oxygen and for sensing gaseous ligands such as oxygen.

Claim 6; Page 10; 94pp; English.

binding protein, HemAT-Hs or HemAT-Bs which reversibly binds oxygen with low affinity. Haem binding protein is useful for controlled storage of oxygen by allowing haem binding protein to bind and store oxygen, and triggering the release of oxygen from haem binding protein by activating the signalling domain. Haem binding protein is useful for sensing gaseous ligands such as oxygen, NO, CO, or CN. Blood substitute comprising haem binding protein is useful for treating a patient suffering from low blood levels by administering and regulating the oxygen binding of the haembinding protein by modifying the signalling domain. Haem binding protein The present invention relates to isolated archeal and bacterial haem

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is useful for haem-based catalysis, for artificial photosynthesis and for identifying potential signalling functions of mutated alpha-haemoglobin and myoglobin causing several diseases. The present sequence is Halobacterium salinarium Hamar-His protein which is salt tolerant. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                      ADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG
                                                                                                                                                                                      ADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG
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                                                                                                                             1 MSNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEAT
                                                                                                                                           MSNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEAT
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                                                                                                                                                                                                                                 KIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEBAAAAVDELVARFLPMLKLLTF
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                                                                                                                                                                                                                                                                           DQQIAMDTYIDSYAQRIHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRART
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                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haem binding protein; HemAT-Hs; HemAT-Bs; gaseous ligand sensor; oxygen storage; artificial photosynthesis; signalling function; alpha-haemoglobin; myoglobin; therapy.
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0
                                                                                      Length 489;
                                                                                                        Indels
                                                                                   Score 2394; DB 4;
Pred. No. 6.3e-165;
0; Mismatches 0;
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                                                                                   100.0%;
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                                                                                                        489; Conservative
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                                                                                              Similarity
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                                                                 Sequence 489 AA;
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The present invention relates to isolated archeal and bacterial haem binding protein. HemAT-Bs which reversibly binds oxygen with low affinity. Haem binding protein is useful for controlled storage of oxygen by allowing haem binding protein to bind and store oxygen, and triggering the release of oxygen from haem binding protein by activating the signalling domain. Haem binding protein is useful for sensing gaseous ligands such as oxygen, NO, CO, or CN. Blood substitute comprising haem binding protein is useful for treating a patient suffering from low blood levels by administering and regulating the oxygen binding protein is useful for treating a patient suffering from low blood levels by administering and regulating the oxygen binding protein is useful for haem-based catalysis, for artificial photosynthesis and for identifying potential signalling functions of mutated alpha-haemoglobin and myoglobin causing several diseases. The present sequence is Bacillus
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                                                                                                                                                                        Novel isolated bacterial heme binding protein, HemAT-Hs or HemAT-Bs which reversibly binds oxygen with low affinity, useful for controlled storage of oxygen and for sensing gaseous ligands such as oxygen.
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cheg 187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.2%; Score 412.5;
26.2%; Pred. No. 1.46
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                                                                                                                                                                                                                                                                                                                             Claim 8; Page 11; 94pp; English
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                                                                    2001-374832/39
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Larsen R;
                                                                                                           N-PSDB; AAD08992
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(first entry)

19-JUN-2003

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Antisense; prokaryotic essential gene; cell proliferation; drug design.
       Protein encoded by Prokaryotic essential gene #23996
                                                21-MAR-2002; 2002WO-US009107
                                                                                (ELIT-) ELITRA PHARM INC.
                       Pseudomonas aeruginosa
                                                                                                    WPI; 2003-029926/02
                                                                                                         N-PSDB; ACA42339
                                WO200277183-A2
                                                               25-OCT-2001;
08-FEB-2002;
                                                        21-MAR-2001;
                                                            06-SEP-2001;
                                                                       06-MAR-2002;
                                       03-OCT-2002
                                                                                         Wang L,
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the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding attisense nucleic acid; (4) an antibody capable of specifically binding che polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that inhibits proliferation or the biological pathway required for cellular proliferation or the biological dentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocit; (10) profiling a compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; in a culture or collection of an expression of the strains is present in a culture or collection of a strains; or (13) identifying the target of a compound that inhibits the screening K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, proliferation of an organism. The antisense nucleic acids are useful for invention relates to an isolated nucleic acid comprising any one of New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. SEQ ID NO 66393; 1766pp; English ftp.wipo.int/pub/published_pct_sequences

Sequence 535 AA;

16; 75; Length Conservative 111; Mismatches 206; Indels DB 6; 16.7%; Score 399.5; DB 6 25.2%; Pred. No. 1.6e-20; Local Similarity Matches 132; Query Match

3 NDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATAD

201 ALVTDFYDHLESYERTQDLFANSTKTVEQ-----LKETQAEYLLGLGRGEYDTEYAAQRA 117 307 SQISDHADNARVISAKSEELASSGGQVILNVVEGMSRIADVVNQSSTSITALGQSSDEIH 366 SVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVE 381 SIIQVIKGIAEQTNLLALNAAIEAARAGEAGRGFAVVADEVRGLAARTTQSTQEITAMIE 426 382 QMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAV 441 --kvvėonoglpindaihoaivei-rpdleayigaaes -----AAAAVDELVARFL-----PMLKLLTFDQQLAMDTY-----IDS--YAQRLHDEI DSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASV EEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVE 187 AGGILVACLVLGQLCRQLLRAVLQPLRKLVSSARVIAQGNLQEPIGVDSNDEAGQLQRAL RIGK-IHDVLGLGPDV--YLGAYTRYYTGLLDALADDV-----VADRGEE 442 STEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485 SENELSVNA-LRNHMEGDMMHD--367 ò g à g ò qq à q ò qq à qq à qq à g

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

2001US-00815242. 2001US-00948993. 2001US-0342923P. 2002US-00072851. 2002US-0362699P.

AAB96493 standard; protein; 739 AAB9649 RESULT

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(first entry) 29-OCT-2001

Putative sensory transduction histidine kinase and response regulator #3 Hyperthermophilic archaeon; hyperthermophilic protein

Pyrococcus abyssi.

R2792651-A1

27-OCT-2000

99FR-00005034. 21-APR-1999; CNRS

99FR-00005034.

21-APR-1999;

IFREMER INST FR RECH EXPL MER CENT NAT RECH SCI CNRS) (IFRE-)

Lecompte 0; Prieur D, Dietrich J, J, Saurin W, Heilig Thierry JC, Weissenbach Forterre P, Querellou J,

VPI; 2001-126236/14.

nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry

Claim 7; Page 1203-1205; 1657pp; French.

The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is

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a hyperthermophilic archaeon, which is isolated from deep-sea hyporthermal vents. The present sequence is one such P, abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centifigrade. Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH775903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AAH775903-AA
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                                                                                                                                                                                                                                                                                                                                                                                            PDVYLGAYTRYYTGLLDALADD------VVADRGEEAAAAVDELVARFLPMLKLLTFDQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LRDIIED--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDRMADVSRE-ISSVSASVEEVASTADDVRRTSE-----DAEALAQQGEAAADDALAT
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                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                            81;
                                                                                                                                                                                                                                                            Length 739;
                                                                                                                                                                                                                                                                                                                                                            83 ANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQ-----RARIGKI---
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                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                         83; Mismatches 150;
                                                                                                                                                                                                                                                         16.2%; Score 387.5; DB 4 28.6%; Pred. No. 1.8e-19;
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2001US-0342923P.
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2002US-0362699P.
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                                                                                                                                                                                                          Sequence 739 AA;
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06-MAR-2002;
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The invention Fracture to an interest actual compilating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits proliferation or the biological pathway required for proliferation. Fequired gene or the biological pathway in which a proliferation required gene or the biological pathway in which a proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibicit; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent or organism or the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of an organism. The antisense nucleic acids are useful for for which each of the strains in cells or conditional drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S aureus, S. typhimurium, cellular proliferation in cells other than S aureus, S. typhimurium, and electronic formar directly from MIPO at the sequence data for this collection of the target procesured the present sequence is encoded by one of the uning in the sequen
                                                                                                                                                                      screening
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                                       J.W.
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                                     Zyskind :
Xu HH;
                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid comprising any
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                                     R, KL
                                       Ohlsen |
Forsyth |
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                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                     66174; 1766pp; English
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27.5%; FLU
                                       Malone C,
Carr GJ,
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les 95; Conservative
ELITRA PHARM INC.
                                       Zamudio C,
Trawick JD,
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The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrochermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAB99143, AAB99143.
    --IGDKIGESV 309
                                                         310 EVTQQGAEVVKTSTEVIKESVSYLTQVAEMMEEMEVKASELREKVIQEGEKIEEGLRFLE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VAVISGALGM-----RLMNSTMRPINEMAKIAESIAEGKLSRAREMVSKIQYREDDE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequences isolated from Pyrococcus abyssi encode proteins
                                                                                                                                                                                                                                                                                            Putative sensory transduction histidine kinase & response regulator #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 L-KLLTFDQQIAMDTY--IDSYAQRLHDEIDSRQELANAVATHV----EAPLSSLEATSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
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                                   ERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMV-
                                                                                                                                                                                                                                                                                                                         Hyperthermophilic archaeon; hyperthermophilic protein.
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W, Heilig R;
                                                                                                               Query Match
15.7%; Score 375; DB 4;
Best Local Similarity 24.4%; Pred. No. 8.6e-19;
Matches 116; Conservative 111; Mismatches 175,
    264 ARAGEAGKGFAVVADEIRKLAEESKKAAEDIRELIKO-
                                                                                            GVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKL
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Weissenbach J, Saurin W,
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IFREMER INST FR RECH EXPL MER.
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                                                                                                                                                                                                   AAB96709 standard; protein;
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Querellou J,
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                                                                                                                                                                               Putative sensory transduction histidine kinase and response regulator #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAV-ATHVEAPLSSLEAT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleotide sequences isolated from Pyrococcus abyssi encode proteins
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----SVEDKEIGGMGAKVROGIED
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Ayperthermophilic archaeon; hyperthermophilic protein.
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Saurin W, Heilig R;
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IFREMER INST FR RECH EXPL MER.
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Weissenbach J, Sau
                                                                                       AAB96483 standard; protein; 435
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les 109; Conserv
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Querellou J,
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              526
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of
                                                                                                                                                                                                       432
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265
                                                                                                                                    LGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQ 372
                                                                                                                                                                    VAEMSKNVGDIINAIADIAEOTNLLALMAIEAARAGELGRGFAVVAQEVRNLAEESKEA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                   248 GMNITADVTQRTVDAMEEFSGVVNEVLSIAREGKDKGEKAISQVEDIQDAMKVIRQAVQE
                                                                                                                                                                                                       STRVEELVEOMOAETEETVDOLDEVNORIGEGVERVEEAMETLOEITDAVEDAASGMOEV
                                                                                                                                                                                                                           368 AEKIRGILNEIQEKVEKAVEETEKGVKVVDDSVDFLKETVGYLMNIGELLDDVESKLQDI
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                                                                                                                                                                                                                                                                                           KNELANTQEHVENAKKALENLAASAQETTASAEEVSASAQEQASSMEEVKRNIIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or efor homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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Yamamoto R, Forsyth RA,
DVAERTDTMR-----ARTDDQVDRMADVSREISSVSASVEEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #27273.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-GCT-2001; 2001US-0342923P.
08-FBB-2002; 2002US-00072851.
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Trawick JD,
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the gene product or that has an activity against a biological pathway consideration, or that inhibits cellular proliferation; (8) athway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising atrains in which the gene compound sactivity; (11) a culture comprising strains in which the gene compound sactivity; (11) a culture compound that inhibits the crown of strains; or (13) identifying the target of a compound that inhibits the crown or strains; or (13) identifying the target of a compound that inhibits the compound that inhibits the compound strains; or (13) identifying the target of a compound that inhibits the compound that inhibits the compound that inhibits the concept of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational crown proximation in cells other than S. aureus, S. typhimurium, C. M. pheumoniae or P. aeruginosa. The present sequence is encoded by one of the traget prokaryotic essential genes. Note: The sequence data for this parent did not form part of the printed specification, but was obtained continual problemat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAFGRDASQFGRVLNGMLEGNATLRITQVEDRDARARLAEIAELFEFVSGSVDEILETS 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AGOISOTMIVIOOTISOT 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :| | :::|||:|| | :|| | 478 GMDNIREQIQDTSKRIKRLGESSQEIGDIVSLIDDIADQINILALNAAIQASMAGDAGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------MDTYIDSYAQRLHDEIDSRQELA---NAVATHVEAPLSSLEATSQDVAERTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLTVTASVTEDFTGAIADSINYSIDQLRELVVTINLTAEQVASAVTETQATAMQLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHD-VLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 ADRIGLDEAEIA----ATADALVTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.6%; Score 374.5; DB 6
24.2%; Pred. No. 1.4e-18;
cive 103; Mismatches 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 PELYQVREASGNIF-NTSQTLLDETSVLANSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acinetobacter baumannii protein #1046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 680 AA;
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ABU40238 standard; protein; 686 AA
                                                                      WPI; 2003-576092/54.
                                                                                                                                                            Query Match
Best Local Similarity
Matches 100; Conserv
                                                              Bush D;
                                                                          N-PSDB; ADA29759.
                                                                                                                                                    Sequence 709 AA;
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                                              09-JUN-1998;
                       JS6562958-B1
                               13-MAY-2003
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                                                                                                                                                                                                                                                      144 LLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDS 203
                                                                                                                                                                                                                                                                                                                  --- DFTGAIADSINFAIDQ 424
                                                                                                                                                                                                                                                                                                                                                              RQELANAVATHVEAPLSSLEATSQDVAERTDTWRARTDDQVDRWADVSREISSVSASVEE 263
                                                                                                                                                                                                                                                                                                                                                                                                                              473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTAT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plants. The present sequence represents the amino acid sequence of an A. baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                      534 SQEIGNIVSLINDIADQTNILALNAAIQASMAGEAGRGFAVVADBVQRLAERSASATKQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 MAQSIDOVSANASESAEVAQRSVQIASNGAQVVNRSIEGMDTIREQIQETSKRIKRLGES
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                       41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLOSASASHIATIMIVVOEITSQITTATFDTARSVSELANMAESLRESV 702
                                                                                                                                             Length 709;
                                                                                                                                                                                                    Indels
                                                                                                                                        15.6%; Score 373.5; DB 6; 28.7%; Pred. No. 1.7e-18; Live 67; Mismatches 141;
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                                                                                                                                                                                                  Conservative
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                          Protein encoded by Prokaryotic essential gene #25765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 68162; 1766pp; English.
                                                                                                                                                                                                                                                 06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342933P.
PEBS-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                        21-MAR-2002; 2002WO-US009107.
                             (first entry)
                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                       Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-029926/02
                                                                                                                    Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACA44108
                                                                                                                                               WO200277183-A2.
                                                                                                                                                                                                                                  21-MAR-2001;
                             19-JUN-2003
                                                                                                                                                                           03-OCT-2002
 ABU40238;
                                                                                                                                                                                                                                                                                                                                                       Wang L,
Wall D,
New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinecobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle of to inhibit A. baumannii infection, and as biocontrol agents for
         Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                           Example, SEQ ID NO 5172; 328pp; English.
                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                     98US-0088701P
                                                                                                                                         99US-00328352
                                                     Acinetobacter baumannii
                      plant biocontrol agent,
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the invention fraction to an institute actual compilating of the nucleic acid inhibits proliferation of a cell. Also included are of the nucleic acid inhibits proliferation of a cell. Also included are coff the nucleic acid inhibits proliferation is inhibited by the antisense appropriate whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated conclined acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or the gene product or that has an activity against a biological pathway or required for proliferation, or that inhibits cellular proliferation; (8) cangound, a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, activity; (11) a culture comparising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the concept of a compound that inhibits the constraints of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains; or (13) identifying the target of a compound that inhibits the collection of collection of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids are useful for collections or for collections or for collections or for collections. K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium The invention relates to an isolated nucleic acid comprising any one of in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

screening

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Sequence 686 AA;

Gaps 75; Length 686; Indels 15.5%; Score 371.5; DB 6; 24.7%; Pred. No. 2.3e-18; iive 91; Mismatches 196; Best Local Similarity 24.79 Matches 119; Conservative Query Match

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-----ADRGEEAAAAVDELVARFLPMLKLLTFDQQIA------MD 187
                                                                                                                                                                                                                                                                                                 424
                                                                                                                                                                                                                                                                                                                         613
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                                                                        290 QTLLDEASHLANG-----FENLAGGRTLDTVG------GYVLGLL-ALASIIL 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense, prokaryotic essential gene, cell proliferation, drug design.
                DIAKRIKRLGESSQEIGDIVSLIDDIADQTNILALNAAIQASLAGEAGFAVVADEVQR
                                                                                                                                                                                                                                                                                                               LSFTGIDD-DTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLF--ANSTKTVEQLK
                                                 ETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVV
                                                                                                                        331 IGLVMVRTTNRQLRETAEKNERNQQAI------MRLLDEIEELADGDLTVTVSVTE
                                                                                                                                                  188 TYIDSYAQRLHDEIDSRQELA---NAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQV
                                                                                                                                                                                                 DRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATD
                                                                                                                                                                                                                         EAVGDMVESIDRVSAHAYESAKVA-----ERSVAIANKGNEVVHNTINGMDNIREQIQ
                                                                                                                                                                                                                                                  305 GVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKA
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                                                                                                                                                                                                                                                                                                                                                                         614 LADLIHSISDAAQLQTSSAGQISHTMAVIQQITAQTSAGSGATADSIRHLARMASEMRRS
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded by Prokaryotic essential gene #35194.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU49667 standard; protein; 644 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342932P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0365699P.
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio cholerae
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                        237
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the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid, (2) a host cell containing the vector; (3) an isolated prolipeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation, or the that has an operon required for proliferation, or that inhibits cellular proliferation; (8) required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required gene or its gene product is compound; a activity, (11) anditure of proliferation of the cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) antibits of a compound that inhibits the compound; a activity; (11) antibits of a compound that inhibits the compound; a conting proteins or screening for homologous nucleic acids required for proliferation of an organism. The antisense nucleic acids required for proliferation of an organism. The antisense nucleic acids required for proliferation of an organism. The antisense nucleic acids required for cellular proliferation in collections of constitution of an organism. The antisense nucleic acids required for proliferation of secreting for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids for cut this cellular proliferation in cells of the present sequence is encoded by one of the target prokaryotic essential genes Note: The sequence dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQA 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 AAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL---DALAD-DVVADR---GEEAAAAVD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGEEVMVASI------YIESMDWFLVGTVPVHEVFAELDAVAQRMMLTTLAVAAIF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 IFMGIFLA-----NSIAMP--INQIAKRFTDLGRGDGDLSQRIEVKGNDEIAQLSKG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADV 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 FNGFIEKIHQSIKDVAQTSRELQVAAEGVSRKALVTHDNSQQQRDQTIQVVTAINQMGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG-LGRGEYDTEY
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  to
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for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                    invention relates to an isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 361; DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 LDEAEIAWRLSFTGIDDDTMAAL----AAEQPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                   1766pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.1%;
                                                                      NO 77591;
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                                                                      25; SEQ ID
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The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF66431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 GRGEYD-TEYAAQRARIGKIHDVL-GLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry.
                                                                                                                                                                                                                                                                ----MRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGE
                                  287 AAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAA
                                                                                                           RAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVE
                                                                                                                                                                                           ---VAEMVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lecompte 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative P. abyssi sensory transduction histidine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                          107 RVEEAMETLQEITDAVEDAASGMOE-VSTATDEQAVSTEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thierry JC, Prieur D, Dietrich J, 1
Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.9%; Score 356.5; DB 4; 26.6%; Pred. No. 1.3e-17; cive 85; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 1066-1067; 1657pp; French.
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IFREMER INST FR RECH EXPL MER
                                                                                                                                                                                                                                                                                                                       GVDDRAGEIAAALDDIADATDQ 473
                                                                                                                                                                                                                                                                                                                                                            866 GVSATFKÉLLÁVAQSLQEÁVKÓ 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 374 AA;
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Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-2001
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(IFRE-)
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535 NQLQNDAKNAVSAMDAGKTVTHQGVAASDEAVQVLMSISDRIHDISDRNTQVATATEEQS 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GP------DVYLGAYTRYYTGLL----DALADDVVADRGEBAAAAVDELVARFLP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention is related to fluorescent apophytochrome-bilin conjugates, known as phytofluors. An apoprotein known as Cph2 from Synechocystis species is used as the apophytochrome and the bilin is preferably phycoerythrobilin. The phytofluors are useful as fluorescent markers for biological research. The phytofluors have a long wavelength shostoption maxima, a high molar absorption coefficient and the recombinant apoproteins can spontaneously assemble with a variety of bilin chromophore precursors. The present sequence is a phytochrome related protein from Synechocystis sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHQCSGPRDWHQNEIDLFGQLTVQVGLALERSDLLAQQKIAE--VEQRQMREKMQKRALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |: | | : : : : : : : | | L--LMEVDPVSRGDLTIRAHV--TEDEIGTIADSYNATIESLRRIVTQVQTAASQFTETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 ADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQP--LFEATADALVTDFYDHLESY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERTODLFANSTKT---VEQLK--ETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived fr
Synechocystis species) and phycoerythrobilin conjugate, useful as
fluorescent markers for biological research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                             ::|| |:|
---KSLRELSGRL 635
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                                    VSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                 Phytochrome, fluorescent apophytochrome, bilin, Cph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.0%; Score 359.5; DB 3; 27.1%; Pred. No. 2.4e-17; tive 86; Mismatches 197;
                                                                                                                                                                                                                                                                                              Synechocystis sp phytochrome-related gene Cph5.
                                                                   TVVHTINQNIEEINAINEVTTSTAEELADAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 48; 52pp; English.
                                                                                                                                                                          AAB26596 standard; protein; 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00272809
                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              WO200056355-A1
                                                                                                                                                                                                                                                                                                                                                                        Synechocystis
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Matches 136;
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense
                                 221
                                                       97
            59
                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                              -EVKLGDLGE-VNELVSRLNNENVKIAEVNDYIQTLSAGIEEMNVQAQQLSDFALESASM
                                                                                                                                        :: ||
-LSKEDEE--
                                 162 AAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSS
                                               22 LEATSODVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEAL
                                                                                                                            AQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNA
                                                                                                                                                                          SIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEOMQAETEETVDQLDEVNORI
                                                                                                                                                                                                                     GEGVERVEEAMETLQEITDAVED------AASGMQEVSTATDEQAVSTEEVAEMVDGVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #8628
                                                                                                                                                                                                                                                                   DRAGEIAAALDDIADATDQQVRTVEEVRETVGKL 488
                                                                                                                                                                                                                                                                               : : : | : | | : | | | KDVSDNLNFATQLTDTISGSLEKLNEVKEEITKL 362
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Haselbeck I
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2001US-0342923P.
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Carr G
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Trawick JD,
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25-OCT-2001;
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pulpeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that thinkis cellular proliferation, (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or underexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                             proliferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at firetive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFAASLDEMMAALERNDDAAYLQLKNVKAGQASAAFAARLGEFSTNLDKLSSETLAAHET 185
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ABU49142 standard; protein; 626

ABU49142

RESULT

(first entry)

19-JUN-2003

ABU49142;

DXXXE

06-MAR-2002; 06-SEP-2001; 21-MAR-2001; 25-OCT-2001;

Antisense; prokaryotic essential gene; cell proliferation; drug design. Protein encoded by Prokaryotic essential gene #34669. 21-MAR-2002; 2002WO-US009107 Vibrio cholerae WO200277183-A2 03-OCT-2002

(ELIT-) ELITRA PHARM INC.

2001US-00815242. 2001US-00948993. 2001US-0342923P. 2002US-00072851.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

WPI; 2003-029926/02 N-PSDB; ACA53012 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 77066; 1766pp; English.

the first manufactures given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated on the polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide, (5) producing the polypeptide, (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway can appear a gene required for cellular proliferation, (8) identifying a gene required for cellular proliferation, (9) identifying a gene required for cellular proliferation of the pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound activity, (11) a culture comprising strains in which the gene compound is activity, (11) a culture comprising strains in which the proventy in whole the compound that inhibits strains in which the proventy in whole its compound is activity.) drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for ceilular proliferation to isolate candidate molecules for rational invention relates to an isolated nucleic acid comprising any one of

Sequence 626 AA;

9 ---AMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSS 14.5%; Score 34%; DB 6; Length 626; 27.4%; Pred. No. 1e-16; .ive 78; Mismatches 134; Indels 32; Gaps Conservative 174 MLKLLTFDQQI--Local Similarity 92; Query Match Matches

298 MSPLKTLDSAIKDIASGGGDLTKKLDTNLDKEFSELALGFNSFTEMLGSQIRQLKTIASG 357 LEATSODVAERIDIMRARIDDQVDRMADVSREISSVSASVEEVASTADDVRRISEDAEAL 281 -QELEQLATAMNEMAMTASEVANSAQVAADA 410 332 EQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETV 391 528 RSMDESKLETDIVVEKTNOVNEKISLVQQAIHRISDMNLQIASAAEEQSLVAREINNNTV 587 282 AQQGEAAADDALATMTDIDEATDGVT-----AGVEQLGE--RAAD-VESVTGVIDDIA 392 DOLDEVNORIGEGVERVEEAMETLQEITDAVEDAASGMOEVSTATDEQAVSTEEVAEMVD 452 GVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGK 487 Search completed: August 10, 2004, 15:26:13 358 VLDGAEKTANEAEVSRLVVEQQL---- $\dot{\delta}$ g δ 셤 ŏ g ð q ò

: 86.6574 secs Job time

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Sequence 23255, A Sequence 32715, A Sequence 32715, A Sequence 30703, A Sequence 23288, A Sequence 2172, Ap Sequence 31724, A Sequence 31724, A Sequence 20097, A Sequence 20097, A Sequence 20092, A Sequence 200
                                                                                                                           August 10, 2004, 15:23:41; Search time 24.8644 Seconds (without alignments) 1015.311 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-31048
US-09-252-991A-28604
US-09-252-991A-26180
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                                                                                                                                                                                                                                                                                                                                                                                 389414 seqs, 51625971 residues
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                                                                                     protein search, using sw model
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Maximum DB seq length: 200000000
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8191. Ap	26639. A		6505, Ap	6739. Ap	24246, A		6560, AD	120, App	28633, A	21242, A	3, Appli	1, Appli	2, Appli	1, Appli	4, Appli	8. Appli	3, Appli
Sequence	Sequence		Seguence	Seguence	Sequence		Sequence	Sequence	Sequence			Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-543-681A-8191	US-09-252-991A-26639	US-08-976-063E-34	US-09-543-681A-6505	US-09-543-681A-6739	US-09-252-991A-24246	US-09-252-991A-31873	US-09-543-681A-6560	US-09-874-923-120	US-09-252-991A-28633	US-09-252-991A-21242	US-08-428-414A-3	US-08-006-676B-1	US-08-282-845-2	PCT-US94-00324-1	US-08-875-435B-4	US-08-973-462-8	US-08-875-435B-3
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552	680	531	519	515	485	452	472	2310	454	107	955	955	955	955	1972	1786	1972
13.1	13.1	12.2	12.0	12.0	11.3	11.0	10.9	10.0	9.7	9.3	9.8	8.5	8.5	8.5	8.2	8.1	8.0
313	313	292.5	288	287.5	270.5	263	261	239.5	231.5	221.5	205	202.5	202.5	202.5	195.5	194	191.5
78	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: MAKE J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,120
NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 ILAMSLPVRHAGOLÍGVAAGDMKLETLTAILNSLKFDGAGYÁFLVSDAGKÍLLHPDSGLV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | : | : | : | | : | | 340 SNDEFGTLANAFNRFVERIHESI---REVAGTA------RQLHDVAQLVVNASNSSMA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EQPVF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------DRG---EEAAAAUDELVARFLPMLKLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TKTVEQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YAAQRARIGKI--HDVLGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 LKTLAEAYPKGAPNIVPGVHEVELDGRSQFVSFTPVKGLPGVTWYVALVLDRDTAYSMLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 TLVTADVRNGIDG-----HALADRIGL----DEAEIAWRLSFTGIDDDTMAALAAEQPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             17.2%; Score 412.5; DB 4; Length 640; 24.4%; Pred. No. 3.3e-24; Live 97; Mismatches 199; Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TRYYTGLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EATADALVTDFYDHL-ESYE-RTQDLFANS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LKETQAEYLLGLGRGEYDTE----
                   Sequence 23252, Application US/09252991A
Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                             GENERAL INFORMATION:
US-09-252-991A-23252
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-23252
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 23252
                                                                                                                                                                                                                                                                                                                                        LENGTH: 640
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Rubenfield et al. NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
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APPLICANT: MATC J. RUBEnfield et al.
APPLICANT: MATC J. RUBEnfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR SILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER: OS 60/094,190
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                                         439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------DRG---EEAAAAVDELVARFLPMLKLLTFDQQIAMDTYID 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESRE 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALNSKTVNIGQILEVIKGISEQTNLIALNAA1EAARAGEAGRGFAVVADEVRNLAHRAQE 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604
                                                                                     494
375 IHSIIQVIKGIAEQTNLLALNAAIEAARAGEAGRGFAVVADEVRGLAARTTQSTQEITAM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKL 488
                                                                     192 SYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSODVAERTDTMRARTDDQVDRMADVS
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                                           380 VEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                440 AVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
                                                                                                                                                            STASDEIAQRVELIAQRSQONTQAMHEMA-AT---ARRLNEVAATM 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%; Score 398; DB 4; L 28.3%; Pred. No. 4.7e-23; tive 74; Mismatches 171;
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US-09-252-991A-32715
US-09-252-991A-32715, Application US/09252991A
Sequence 32715, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
THILE OF INVENTION: NUCLEIC ACID AND AW
                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
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US-09-252-991A-23255
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALVTDFYDHLESYERTQDLFANSTKTVEQ-----LKETQAEYLLGLGRGEYDTEYAAQRA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AAAAVDELVARFL----PMLKLL-----TFDQQIAMDTYIDSYAQRLHD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTWRARTDDQVDRMADVSREISSVSA 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 NISQISDHADNARVISAKSEELASSGGQVILNVVEGMSRIADVVNQSSTSITALGQSSDE 374
                                  299 IDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVV 358
                                                                                                                                                                                 ADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEI 418
                                                                                                                                                                                                               TDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTV 478
                                                                                                                                                                                                                                                                                                               TSRIGEIDSMNÓSVATATBEÓTA-----VVDSLNMDITEINTLNOEGVENLQATLRAC 621
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      RIDDOVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMID 298
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                                                                                                                     3 NDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.8%; Score 401.5; DB 4; Best Local Similarity 24.9%; Pred. No. 1.9e-23; Matches 131; Conservative 111; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31086, Application US/09252991A, Patent No. 6551795
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US-09-252-991A-31086
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LENGTH: 545
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                            59 ATADALVIDFYDHLESYERIQDLF----ANSTKIVEQLKEIQAEYLL----GLGRGEYD 109
                                                                                                                                                                                                                                                                                                                270 -----FVSGSVD--EILETSPDLFQVREAANNIFSVSQTILLDKASQLADGFENLAGGRSI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                587 NEAVISMEQTISEVVRGARLAQDAGVALEEIEKVSKTLAALIQNISNAARQQASSAGHIS 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAET 387
                                                                                                                                                                                           1 MSNDNDTLVTADVRNGIDGHALADRI--GLDEAEIAWRLSFTGIDDDTWAALAAEQPLFE
                                                                                                                                                                                                                             213 LAGDENSVQAAD-SFGRDA-SLFGRVLKGMQEGNAAMSISKV-TNAEAVDRLNEIAELFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 --LADGDLTVAATVTE------DFIGALADSINYSIDQLRELVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 NLFA-----GYVLGALALASIILIGLVMVRETNRRLAETABKNDRNQAAILRLLDEIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                            151 DVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 -NAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVAST
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                                                                                                                                                         79;
                                                                                                                 Length 696;
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                                                                                                                                                         Indels
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                                                                                                            ; Score 389.5; DB 4;
; Pred. No. 2.3e-22;
98; Mismatches 210;
                                                                                                                                                                                                                                                                                                                                                           110 TEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTG--
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                     TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-16965
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SEQ ID NO 32789
LENGTH: 710
                                                                                                          Query Match
Best Local Similarity 25.3
Matches 131; Conservative
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Best Local Similarity
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                         79 QDLFANSTKTVEQLK-----ETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPD
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                                                                                                                                                                                                                                                                                                                                                   87; Mismatches 158; Indels 147;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                Length 906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 VYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLL----
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                                                                                                                                                                                                                                                                                                            16.6%; Score 397.5; DB 4 24.8%; Pred. No. 7.9e-23;
                 FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-07-27
NUMBER: SEQ ID NOS: 33142
LENGTH: 906
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
FRIOR FILING DATE: 1998-07-27
SEQ ID NO 16965
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Best Local Similarity
Matches 129; Conserv
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Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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              -TSEDAEALAQQGEAAADDALATMTDIDEATDGV 306
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                                                                                                                                                                               DMNPQIASAAEEQSAVAEDINRNVANIGQVANQVAGGADEASQASAELTRLAEQQRRLVN 730
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                                                                                      TAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALA
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                                                491 IELVATAVHEMTATAQDVARNATHAAEAANHADQAAHQGKQIVESSSAAIQALASEIGRA
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APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AN TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIF FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23956
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Best Local Similarity
Matches 141; Conserv
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Patent No. 6551795

GREERAL INFORMATION:
GREERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30703

LENGTH: 734
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                                                                                                                                                                                                                                                                                                                                                                 EELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTAT 436
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TKTVEQLKETQAEYLLGLGR-----GEYDTEYAAQRARIGK-IHDVLGLGPDVYLG-AYT 138
                                                                                                                             RYYTGILD-ALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRL 197
                                                                                                                                                                                                                                    421 MORMGDSLRELVGRIGDGV----SOLASSAEELSAVTEQTRAGVNSOKVETDQVATAMHE 476
                                                                                                                                                                                                                                                                       VSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGER 316
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                                                                                                                                                                                                                                                                                                  ---GOLORV
                                                                                                                                                                                                                                                                                                                                                                                                                                          198 HDEI-DSROELANAVATHVEAPLSSLEATSODVAERTDTMRARTDDOVDRMADVSREISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGK 487
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                                                                                                                                                             377 ROIVRPLDEALA-----OAEALAAGDLGKRPONPLTLORRDEL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%; Score 380.5; DB 4; 24.7%; Pred. No. 1.3e-21; ive 91; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GIDDDIMAALAAEQPLFEATADALVTDFYDHLESY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30703
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Best Local Similarity 24.7%
Matches 119; Conservative
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US-09-252-991A-30703
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PARLET NO. 35.1793

APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VSRIHETSQEVARYTQDTQSITNQLAEASEHQAQEIAGASTAMNE 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 VASTADDV-RRTSEDAEA----LAQQGEAAADDALATMTDIDEATDGVTAGVEQLGER 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 AADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELVEOMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTAT 436
                                                                                                                                                                                                                                                                                                                                                                ---- DFTGAIADSINFAIDQ 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 ETLVKTIQTDTNEAVISMEQTTTEVVRGANLAKDAGIALDEIQKVSGDLAKLIASISDAA 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---VADR- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 LLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LDEAEIAWRLSFTG-IDDDTMAALAAEQPLFEA
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                                                                                                                                                                                                             Length 709;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 DEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV
                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                           Query Match 15.6%; Score 373.5; DB 4; Best Local Similarity 28.7%; Pred. No. 4.3e-21; Matches 100; Conservative 67; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31412, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                388 LLDEIAD--LADGDLRSYATVSE---
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                                                                                                          TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
          CURRENT FILING DATE: 1999-06-04
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Matches 142; Conservative
                          NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5172
LENGTH: 709
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LENGTH: 614
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NO. 1931 193

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERCHGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23288
LENGTH: 701
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                                                                                                             158 BEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEA 217
431 --HKLHDVSQLVVNASNSSMANSDEQSNRTNSVAAAINELGAAAQEIARNAADASHHASD 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 NQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 VEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQ 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 PLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSED
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                                                                                                                                                                                440 AVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
                                                                                                                                                                                                                   SAVAEEINRSVTAIREVADQSAQAMQSTASSSEQLAELGRELQGMV 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
15.8%; Score 379; DB 4; Length 701;
Best Local Similarity 29.0%; Pred. No. 1.6e-21;
Matches 96; Conservative 67; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 GEIAAALDDIADATDQQVRTVEEVRETVGKL 488
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                                                                                                                                                                                                                                                                                                                                                           ; Sequence 23288, Application US/09252991A
; Patent No. 6551795
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US-09-252-991A-23288
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Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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ADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVI 327
                                                                                                      DDIAEQTIMILALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAET 387
                                                                                                                                                   KGIAEQTNLLALNAAIEAARAGEQGRGFAVVADEVRALAARTQDSTKDIQARIERLQAGV 470
                                                                                                                                                                                                         EETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVA 447
                                                                                                                                                                                                                                                            .---- G 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 ALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AAIRDVTESLSSQAEESAQVSQ 742
                                  454 ORLPHTGRDELGELAGWFNRFLDKLOPIIRDVKVSVRDARSTADOSAAISSQTSAGMQQQ
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                                                                                                                                                                                                                                                          ---AAGVDGVLAAT----
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31.7%; Pred. No. 1.8e-20;
iive 61; Mismatches 126;
                                                                                                                                                                                                                                                                                                             EMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31724, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF OF INVENTION:
TOTAGE APPLICATION OF THE OF OF THE OF
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US-09-252-991A-25899
; Sequence 25899, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    694 VINDMNLQIASAAEEQSSVAEEINRNV-
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SLNRLA 748
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US-09-252-991A-31724
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APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260
                                                                                                261 MLLGSLVLIGASLAVALLSLWLVNRNLVRPVQRLIEHIAQLSHGDFGERIEIRRKDELGK 320
                                                                                                                                                                                    VSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGER 316
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                                                   -----GEEAAAAVDE--LVARFL--PMLKLLTFDQQIAMDTYIDSYAQRLHDEIDS
                                                                                                                                                      204 RQELANAVATHVEAPLSSLEATSQDVAERTDT------MRARTDDQVDRMADVSREISS
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Pred. No. 7.9e-21;
89; Mismatches 175;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
SEQ ID NO 18744
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207 RQRF---
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US-09-252-991A-18744
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US-09-252-991A-18744
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Patent No. 6605709
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-01
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR PELING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
           TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TADALVTDFYDHLESYERTQD----LFANSTKTVEQLKETQABYLLGLGRGEYDTEYA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 AQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLP 173
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                                                                                                                                                                                                                                                                                                                    Length 613;
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26.9%; Pred. No. 3.3e-20;
Live 75; Mismatches 204;
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                                                                                                                                                                                                                                                                                                                                                                                               19 GHALADRIGLDEAEIAWRLSFTGIDD-
Marc J. Rubenfield et al.
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; ORGANISM: Proteus mirabilis
US-09-543-681A-6665
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Matches 129; Conserv
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LENGTH: 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 LDEVNQRIGEGVERVEBAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGV 453
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; Score 359; DB 4; Length 579;
; Pred. No. 4.4e-20;
85; Mismatches 181; Indels 114;
                                                                                                                                                                                                                                      101 LGLGRGEYDT---EYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL
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   15.0%;
   Query Match 15.05
Best Local Similarity 25.95
Matches 133; Conservative
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Bank

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August 10, 2004, 15:28:46; Search time 71.0412 Seconds (without alignments) 2159.184 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/USOOB.PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2394
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Perfect score:
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                                                                                                                                                                                     OM protein
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                                                                                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	33, A	App	74, A	69670, A	52, A	31, A	pli	25, A	App	56, A	35, A	Appl	78, A)2, A	54, A
d	663	531,	6617	1969	6816	7759	5, Ar	5102	372,	7706	523	28,	772	176	6956
Description	Sequence 66393, A	Sequence 531, App	Sequence 66174, A	Sequence	Sequence 68162, A	Sequence 77591, A	Sequence 5, Appli	Sequence 51025, A	Sequence 372, App	Sequence 77066, A	Sequence 52305, A	Sequence 28, Appl	Sequence 77278, A	Sequence	Sequence 69564,
ΠD	US-10-282-122A-66393	US-10-389-647-531	US-10-282-122A-66174	US-10-282-122A-69670	US-10-282-122A-68162	US-10-282-122A-77591	US-09-272-809-5	US-10-282-122A-51025	US-10-389-647-372	US-10-282-122A-77066	US-10-282-122A-52305	US-10-332-288-28	US-10-282-122A-77278	US-10-282-122A-77602	US-10-282-122A-69564
	12	12	12	12	12	12	σ	12	12	12	12	12	12	12	12
% Query Match Length DB	535	535	682	089	989	644	891	539	619	626	989	547	641	643	501
% Query Match	16.7	16.7	16.1	15.6	15.5	15.1	15.0	14.9	14.6	14.5	14.1	13.9	13.6	13.2	13.1
Score	399.5	399.5	386.5	374.5	371.5	361	359.5	356.5	348.5	348	338	332	326	315	314.5
Result No.	-	71	m	4	2	9	7	6 0	6	10	11	12	13	14	15

2A-77047 Sequence 77047, A	17	3-34 Sequence 34, Appl									0							m	-6249	120	20 Sequence 120	-114 Sequence 11	13 Sequence 11	546 Sequence 18	1 Sequen	-6246 Sequence 6246,		-10395 Sequence 10399
US-10-282-122A-77047	US-10-282-122A-76517	US-08-976-063C-34	08-09-750-986	US-10-335-977	US-10-335-977	US-09-882-227-4	US-09-882-227	US-10-335-977	US-10-335-977	US-10-335-977-4943	US-10-282-122	US-10-389-647	US-10-012-819-228	US-08-945-038-	US-10-335-977-8500	US-10-335-977	US-10-369-493	US-10-282-122	-97	US-09-874-923-	US-09-991-496-120	US-09-820-843A	US-09-820-843A-1	0-369-	US-10-243-552	0-335-	US-10-156-761	
12	12	8	11	12	12	10				12		12	12	80	12	12	15	12		σ	σ	10	10	15	12	12	14	
541	845	531	531	564	564	265	630	675	293	664	753	431	431	433	433	438	883	654	673	2310	2310	2310	2354	1190	266	202	1258	
13.1	12.9	12.2	12.2	12.2	12.1	12.1	11.9	11.7	11.5	11.4	11.2	11.0	10.7	10.6	10.5	10.5	10.2	10.1	10.1	10.0	10.0	10.0	7.6	9.4	9.5	9.1	6	
313.5	308	292.5	292.5	292	289	289	284	280	276	273.5	269	263	257	254	252.5	252.5	245	241	241	239.5	239.5	239.5	231.5	225	221	217.5	212	1
16	17	18	13	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	,

ALIGNMENTS

TITLE OF INVENTION. Identification of Essential Genes in Microorganisms
TITLE REFERENCE: ELITAA.034A
; TITLE REFERENCE: ELITAA.034A
; CURRENT APPLICATION UNDERS: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION UNDERS: 60/191,078
; PRIOR PILING DATE: 2000-03-21
; PRIOR PILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-66
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR PILING DATE: 2000-10-23
; PRIOR PILING DATE: 2000-10-23
; PRIOR PILING DATE: 2000-110-23
; PRIOR PILING DATE: 2000-110-23
; PRIOR PILING DATE: 2000-11-27
; PRIOR PILING DATE: 2000-11-22
; PRIOR PILING DATE: 2000-11-22 ; Sequence 66393, Application US/10282122A ; Publication No. US20040029129A1 ; GENERAL INFORMATION: APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R. APPLICANT: APPLICANT:

a

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; TYPE: PRT
; ORGANISM: Pser
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                                                                                                                                                                                                                                                                                                               -----ALRADVLAAFVV-QPGDGAAAE
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            PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 66393
                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                            Length 535,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GREENERG, E. Peter
APPLICANT: GREUNEER, Martin
APPLICANT: GRUNTER, Martin
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
SOFTWARE: FSELSEQ for Windows Version 4.0
SEQ ID NO 531
LENGTH: 535
                                                                                                                                                                                                                        Best Local Similarity 25.2%; Pred. No. 1.8e-18;
Matches 132; Conservative 111; Mismatches 206; Indels
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                                                                                                                                                                                                            DB 12;
                                                                                                                                                                                                          16.7%; Score 399.5; DB 1
25.2%; Pred. No. 1.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 531, Application US/10389647; Publication No. US20040033549A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             SENELSVNA-LRNHMEGDMMHD
                                                                                                                                                       : Pseudomonas aeruginosa
FILING DATE: 2001-02-09
                                                                                                                                                           ; UKGANISM: FREULU
US-10-282-122A-66393
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                                                                                                                                     TYPE: PRT ORGANISM:
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79 QVRQDLQEHSQWFR------KVVEQNQGLPLNDAIHQALVEL-RPDLEAYIGAAES 127
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                                                                                                                                                                      3 NDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATAD
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                                                                                                                        75;
                                                                          DB 12; Length
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                                                                                                                        Indels
                                                                                                                     Mismatches 206;
                                                                     Score 399.5; DB 1
Pred. No. 1.8e-18;
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66174, Application US/10282122A
Publication No. US20040029129A1
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                     Conservative 111;
Pseudomonas aeruginosa
                                                                     16.7%;
25.2%;
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APPLICANT: Zamudio, Carlos
APPLICANT: Halone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto, Robert
Forsyth, R.
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Carr, Grant
                                                                     Query Match
Best Local Similarity
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                                                                                                                   Matches 132;
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LENGTH: 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 VEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADV 320
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 VSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
                              PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR PRIOR PRIOR DATE: 2001-02-16
PRIOR PRIOR PRIOR DATE: 2001-02-16
PRIOR PRIOR PRIOR DATE: 2001-02-16
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APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Tamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: Olsen, Kari
APPLICANT: Nall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
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15.6%; Score 374.5; DB 12; Length
Best Local Similarity 24.2%; Pred. No. 1.1e-16;
Matches 120; Conservative 103; Mismatches 201; Indels
PRIOR PALICATION NUMBER: 60/206, 848
PRIOR PELICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PELICATION NUMBER: 60/230, 347
PRIOR PELICATION NUMBER: 60/230, 347
PRIOR PELICATION NUMBER: 60/242, 578
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/257, 931
PRIOR PILING DATE: 2000-12-22
PRIOR PELICATION NUMBER: 60/267, 636
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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; Sequence 68162, Application US/10282122A
; Publication No. US20040029129A1
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US-10-282-122A-69670
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TITLE OF INVENTION: Identifi
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                                                                                                                                                                                                                                                                                                      RESULT 6
US-10-282-122A-77591
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SEQ ID NO 77591
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Matches 120;
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                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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NUMBER OF SEQ ID NOS: 78614
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QTLLDEASHLANG-----FENLAGGRTLDTVG-
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-06
PRIOR PELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,579
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-12-20
Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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ORGANISM: Pseudomonas putida
                                                                                                                                                                                                          Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 24.77
Matches 119; Conservative
                                                                                                                                      Wall, Daniel
Trawick, John
Carr, Grant
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365 LAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVED 424
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                                               ||||| :::| || || ::| || ::| || ::
554 LAERSSSATRQIEALVRTIQADTNEAVISMEQTTAEVVRGARLAQDAGVALAEIEGVSQN
                                                                                                                                       425 AASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRET
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 60/20,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,93
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-12-02
PRIOR FILING DATE: 2001-12-02
PRIOR FILING DATE: 2001-12-03
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
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Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
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347 RAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVE 406
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CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT PELLING DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/2030,335
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/257,931
PRIOR PELICATION NUMBER: 60/257,931
PRIOR PELICATION NUMBER: 60/257,636
PRIOR PELICATION NUMBER: 60/267,636
                                                                                                                 627 DINEVAVRQLAQQANRQALDVAEALERLQAMNKSIQAVAENAAQAESAVQRATQTVDQGE
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                                                                                                                                                                                      287 AAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAA
                                                              DT------MRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGE
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SEQ ID NO 51025
LENGTH: 539
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Zyskind, Judith
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APPLICANT:
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APPLICANT:
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                                                                                                          113 AAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL---DALAD-DVVADR----GEEAAAAVD 165
                                                                                                                                                                   ----YIESMDWFLVGTVPVHEVFAELDAVAQRMMLTTLAVAAIF 304
                                                                                                                                                                                                                                                                                           ----NSIAMP--INQIAKRFTDLGRGDGDLSQRIEVKGNDEIAQLSKG 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 AHQCSGPRDWHQNEIDLFGQLTVQVGLALERSDLLAQQKIAE--VEQRQMREKMQKRALE
                      199 SFKIEDTGFVFLINAQGEVQIHRQKEQV----KSSLQQIYGSGASALLNKSGFNLISTDY
                                                                                                                                                                                                                                                                                                                                                                                                            355 FNGFIEKIHQSIKDVAQTSRELQVAAEGVSRKALVTHDNSQQQRDQTIQVVTAINQMGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 ESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELV
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                                                                                                                                                                                                                                     -EIDSROELA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5. Application US/09272809
Patent No. US200202239A1
GENERAL INFORMATION:
APPLICANT: Lagarias, John C.
TITLE OF INVENTION: Phytofluors as fluorescent labels
FILE REFERENCE: 2500.1180S0
CURRENT APPLICATION UNBER: US/09/272,809
CURRENT FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                     166 ELVARFLPMLKLLTFDQOIAMDTYIDSYAQRLHD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                       305 IFMGIFLA---
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ORGANISM: Unknown
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Best Local 1
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APPLICANT: APALLANI, JUGILIA
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
ITILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERRICE: ELITRA.034A
CURRENT APPLICATION NUMBER: 06/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/203,21
PRIOR PLING DATE: 2000-05-26
PRIOR PPLING DATE: 2000-05-26
PRIOR PPLING DATE: 2000-05-26
PRIOR PPLING DATE: 2000-05-26
PRIOR PPLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-01-23
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-01-23
PRIOR PPLING DATE: 2000-01-23
PRIOR PPLING DATE: 2000-01-23
PRIOR PPLING DATE: 2000-11-27
PRIOR PPLING DATE: 2000-11-27
PRIOR PPLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
               135 GAYTRYYTGILDALADDVVADRGEEAAAAVDELVARFLPMLKLLIFDQQIAMDTYIDSYA 194
                                                 ORLHDBIDSROBLANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREI 254
                                                                                                                                                                 OLKDFSNDTAÖSLSRMLGOIREA-ADTINTAASEIASGNAELSARTEOOASSLEETASSM 426
                                                                                                                                                                                                                  255 SSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMIDIDEAIDGVIAGVEQLG 314
                                                                                                                                                                                                                                                                                                                                                 315 ERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQST 374
                                                                                                                                                                                                                                                                                                                                                                                                                  375 RVBELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVST 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 EIKTLIS------DSVDKVE----NGNTLVAQAGQTMSDIVVAIRRVTDIMSELAA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 AIDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKLS 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 77066, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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ORGANISM: Vibrio cholerae
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US-10-282-122A-77066
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LENGTH: 626
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                                                                                                                                                                                                KETOAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDV 152
                                                                                                                                                                                                                                                                                                153 VADRGEBAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVA 212
                                                                                                                                                                                                                                                                                                                                               213 T--HVEAPLS-----SLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSA 259
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                                                                                                38 SFTGIDDDTMAAL----AAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 STRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEV 432
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                                                                                                                                                                                                                               253 ALRHMQESLTRTVAAVRRGVDEINVGSREISAGNTDLSSRTEEQ-----AASLEETÄA
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Mismatches 153; Indels 113;
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       DB 12; Length 539;
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Publication No. US20040033549A1

GENERAL INFORMATION:
APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
ITILE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REPRENCE: UIZ-036CP
CURRENT PILIGN NUMBER: US/10/389,647

CURRENT PILIGN DATE: 2003-03-14

PRIOR APPLICATION NUMBER: 09/653730

PRIOR APPLICATION NUMBER: 60/153022

PRIOR PILING DATE: 2000-09-01

PRIOR PILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 710

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH. 2000

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LENGTH. 2000

SOFTWARE: FastSEQ for Windows Version 4.0
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                                 Pred. No. 1.3e-15;
     14.9%; Score 356.5; 26.6%; Pred. No. 1.3
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                                                   Conservative
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Best Local Similarity 25.9
Matches 123; Conservative
                       Similarity
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US-10-389-647-372
                                              126;
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US-10-389-647-372
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Query Match
Best Local
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                                                 Matches
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Query Match
Best Local Similarity
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                                                                                                                                                     298 MSPLKTLDSAJKDIASGGGDLTKKLDTNLDKEFSELALGFNSFTEMLGSQIRQLKTIASG 357
                                                                                                                                                                                                                                                                                                        392 DQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVD 451
                                                                                                                                                                                             222 LEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRISEDAEAL 281
                                                                                                                                                                                                                                                                                AQQGEAAADDALATMTDIDEATDGVT-----AGVEQLGE--RAAD-VESVTGVIDDIA 331
                                                                                                                                                                                                                                                                                                                                                               EQTINMLALMASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEOMQAETEETV 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAR.034.
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                ----AMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSS
                                                                          Gaps
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PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
                                                                            32;
                                    Length 626;
                                    14.5%; Score 348; DB 12; Length 6
27.4%; Pred. No. 5.7e-15;
ive 78; Mismatches 134; Indels
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PRIOR PLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-26
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
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PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-27
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PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-2
PRIOR PLING DATE: 2000-12-2
PRIOR PLING DATE: 2000-12-2
PRIOR PLING DATE: 2000-12-2
PRIOR PLING DATE: 2000-12-2
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
                                                           Best Local Similarity 27.4
Matches 92; Conservative
                                                                                                                       174 MLKLLTFDQQI-
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US-10-282-122A-77066
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                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 LTFDQQIAMDTYIDSYAQRLHDEIDSRQBLANAV-----ATHVEAPLSSLE---ATSQ 227
                                                                                                                                                                                                                                                                                                                                                                   350 LTEKVEIVNEDEIGKLSKIFNTMIDSLREITRNINNFSIQLAGSSQEILSSAEQTSAVSE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::: |::: || :: || :: | 410 EISSATEETASGAENQVKASNESSLLMNDVMGNMYTLKEEFDEIISFSNNTNTLASKGQE 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: RAINEY, Paul Barton
APPLICANT: SPIRSS, Andrew Julien
APPLICANT: SPIRSS, Andrew Julien
APPLICANT: SPIRSS, Andrew Julien
APPLICANT: SPIRSS, Andrew Julien
APPLICANT: BANTHNAKI, Eleni
TITLE OF INVENTION: BACTERIAL POLYSACCHARIDE AND BIOFILM DEVELOPMENT
FILE REFERENCE: 10317.700120500
CURRENT APPLICATION NUMBER: US/10/332,288
CURRENT FILING DATE: 2003-10-06
PRIOR PRING APPLICATION NUMBER: PCT/GB01/03077
PRIOR APPLICATION NUMBER: US/006842.7
PRIOR PILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 AADDALAIMIDIDEAIDGVIAGVEQLGERAADVESVIGVIDDIAEQINMLALNASIEAAR
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                                                                                                                                                                                                                                                                         80; Mismatches 130;
                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                    14.1%; Score 338; DB 1
26.8%; Pred. No. 3e-14;
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US-10-332-288-28
                                                                                                              TYPE: PRT ORGANISM: Clostridium botulinum
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 52305
LENGTH: 686
                                                                                                                                                                                                                                                                               91; Conservative
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                                                                                                                                                                                                                               99 YLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDAL-ADDVVADRG 157
                                                                                                                                                                                                                                                                                                                      158 EEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEA 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 PLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSE-
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                                                                                                                                           DIWAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAE--
                                                                                                      Indels 108;
                                                               Length 641;
                                                                                                                                                                                                                                                                                                                                                             301 QEQSAACEE----SLKSLD-QQQIALDGAVTA-AQSLDELTDELR--
                                                           ; Score 326; DB 12; ]; Pred. No. 1.7e-13; 97; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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PRIOR PEDLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                    Query Match
Best Local Similarity 24.1%
Matches 117; Conservative
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Yamamoto, Robert
Forsyth, R.
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             US-10-282-122A-77278
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                                    196 ISMAVSLLIAILAAGLCGLLLMRAIMAPMQRIVDI----LETWRDGDLSKRLNLERKDE 250
                                                                                  201 IDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSAS 260
                                                                                                                  311 SREIAATSKOLVRIMTEVSTAADQASVAAGSGQQGLARMEETMHSVMGAADLVNAKLAIL 370
           ---DE 200
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CURRENT APPLICATION UNBER: US/10/282,122A
CURRENT FILING DATE: 2003-20-20
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  -ARFLPMLKLLTFDQOIAMDTYID-SYAORLH-
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-10-02-09
PRIOR PILING DATE: 2001-02-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Yamamoto, Robert
Forsyth, R.
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Trawick, John
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LENGTH: 641
TYPE: PRT
ORGANISM: Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 YLGIEFDGYYKRV--NLTDDMYWILMVFVDKA-TALADVDVAVANAITTGIVLIGISVGV 305
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                        PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-04
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-03
PRIOR PELING DATE: 2001-02-03
PRIOR PELING DATE: 2001-02-03
PRIOR PELING DATE: 2001-02-03
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                                                                                                                                                                                                                                                                                                                                                                                                                             13.2%; Score 315; DB 12; Length 643; llarity 24.9%; Pred. No. 9.2e-13; Conservative 77; Mismatches 167; Indels 58
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FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Vibrio cholerae
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Matches 100; Conserv
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US-10-282-122A-69564
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LENGTH: 643
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278 AEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNML 337
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CURKENI FILLING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-05-26
PRIOR PRIOR PLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-09
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ORGANISM:
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Matches 8
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Bank

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Search time 21.3123 Seconds (without alignments) 2207.061 Million cell updates/sec August 10, 2004, 15:22:45; Run on:

US-09-455-978B-2 2394 1 MSNDNDTLVTADVRNGIDGH.....AIDQQVRIVEEVRETVGKLS Title: Perfect score:

BLOSUM62 Scoring table: Sequence:

283366 segs, 96191526 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* 1264 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	transducer protein			transducer protein	Htr3 transducer [1	transducer protein	Htr18 transducer		transducer protein	transducer protein		halobacterial tran	transducer protein	sensory rhodopsin	Htr15 transducer			transducer protein	Htr8 transducer [1	Htrl6 transducer	Htr7 transducer [1	halobacterial tran		transducer protein			transducer protein		transducer protein
SUPPLEMENTES	Ω	T44978	E84304	A84294	T44973	HB4336	T48840	B84238	23	T48897	T44849	F84327	T46810	T44597	S55299	A84252	T44606	T44964	T44938	H84305	F84219	E84327	681	$^{\circ}$	T44262	C84298		49	4	T44276
	DB	2	~	7	7	7	7	7	7	7	7	7	~	7	~	~	7	7	7	7	7	•	~	•				~1		7
	Length	489	489	481	482	633	805	790	778	778	452	810	810	777	534	989	804	451	544	643	628	545	545	789	788	420	642	773	627	419
	% Query Match	100.0	98.	9	ഗ	24.9	24.9	24.2	24.1	23.9	23.4	23.2	23.1	22.6	22.5	22.4	22.1	21.9	21.9	21.9	21.8	21.8	21.8	21.3	21.2	21.1	21.1	21.0	20.9	20.8
	Score	2394	2360	643	609.5	597	597	580	578	573	560.5	555	554	540.5	537.5	535.5	529	524	523.5	523.5	521.5	521	521	509.5	507.5	506	505	502.5	499.5	497.5
	Result No.		10	ım	4	Ŋ	9	7	00	0	10	11	175	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Htrl7 transducer [methyl-accepting c	Htr2 transducer [i	transducer protein	Htrl transducer [i	transducer protein	Htrl3 transducer [transducer protein	methyl-accepting c	methyl-accepting c	methyl-accepting c	methyl-accepting c	chemotactic transd	methyl-accepting c	methyl-accepting c		mernyl-accepting c
D84325	C87302	A84328	A47190	E84318	T44946	H84257	T44258	G84132	D87536	A83713	C69832	H83106	A97485	AR2703		D84137
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536	537	764	536	536	765	423	423	559	555	439	432	632	499	004	1	579
20.8	19.9	19.4	19.4	19.4	. 61	18.6	18.4	17.5	17.3	17.3	17.2	17 1	10.7		0.11	16.9
497	475.5	464	463 5	463.5	1001	45.2	439.5	419.5	415	413	412.5	409.5	40.4	000	400	405.5

ALIGNMENTS

RESULT 1		
T44978		
March Contract	The total	Lond

T449/0

Transducer protein hemAT [validated] - Halobacterium salinarum
NiAlternate names: methyl-accepting taxis protein htB; transducer protein htB; transducer
Species: Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Accession: T44978
R;Zhang, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.
R;Zhang, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.
R;Zhang, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.
A;Ccession: T44978
A;Title: Signal transduction in the archaeon Halobacterium salinarium is processed throw
A;Reference number: Z22804; MUID:96209786; PMID:8643458
A;Rocession: T44978
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T44978
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 «ZHA»
A;Status: preliminary
A;Cross-references: Strain Flx15
A;Cross-references: Strain Flx15
A;Cross-references: Strain Flx15
A;Genetics:
C;Genetics:
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Halobacterium salinarum transducer protein htrl
C;Superfamily: Halobacterium salinarum transducer protein htrl
C;Superfamily: methylated amino acid; signal transduction

ö 09 Gaps 0; Length 489; Indels tch al Similarity 100.0%; Score 2394; DB 2; al Similarity 100.0%; Pred. No. 7.8e-98; 489; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 489; Conservi

9 1 MSNDNDTLVTADVRNGIDGHALADRIGLDBAEIAWRLSFTGIDDDTMAALAAEQPLFEAT q à

61 ADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG 120 à g

121 KIHDVIGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTF

ò

180

240 181 DQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRAKT 121 g ð

241 DDQVDRWADVSREISSVSASVEEVASTADDVRRTSEDABALAQQGBAAADDALATMTDID 300 181 g ò

301 EATDGYTAGYEQLGERAADVESYTGYIDDIAEQTNMLALNASIEAARAGEAGEGFAVYAD 360 g g ò

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74 SYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 LGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLL-----TFDQQI--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 FIATPVYHTGEFRGVI-EIVODR-SSSARYOSELQALFGELVDTLDAYDAGRFDATVDIA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transducer protein htpIII [similarity] - Halobacterium salinarum
N;Alternate names: methyl-accepting taxis protein htk; transducer protein htk;
C;Species: Halobacterium salinarum
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 NGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATADAL-VTDFYDHLE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 SVTSDVEALQNRIEDIDEVVDVITGIAEQTNMLALNASIEAARAGEEGEGFAVVAEEVKA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVED 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 AASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRET 484
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                                                                                                      'Species: Halobacterium sp. NRC-1
Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D----DGSRALANKVADTPIDAHHEY----DGVGLADESYALLTGDYVYEDTTVAGNTDLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 481;
                                                                                                                                                                                                                                                                                                                                                   A;Gene: htr9
C;Superfamily: Halobacterium salinarum transducer protein car
                                                                                                                                                                                                                                                                                                                                                                                                   26.9%; Score 643; DB 2; L
37.6%; Pred. No. 2.1e-21;
ive 72; Mismatches 196;
                                                                                    Htr9 transducer [imported] - Halobacterium sp. NRC-1
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Query Match
Best Local Similarity
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VSEL 478
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R; My W. Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable J. Jung, K.H.; Alam, M.; Freitas, T. Zoraz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Atticle: Genome sequence of Halobacterium species NRC-1.
A; Accession: E84304
A; Molecule type: DNA
A; Residues: 1-489 cSTO>
A; Accession: E84304
A; Molecule type: DNA
A; Estatus: Preliminary
A; Molecule type: DNA
A; Cross-references: GB-AE004437; NID:g10580997; PIDN:AAG19801.1; GSPDB:GN00138
C; Genetics:
A; Genetics: A; Generic and Allopacterium salinarum transducer protein htrl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Species: Halobacterium sp. NRC-1
;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                   BVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITD
                                                            AVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEE
                                                                                        AVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSNDNDTLVTADVRNGIDGHALADRIGLDEABIAWRLSFTGIDDDTWAALAAEQPLFEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2360; DB 2;
Pred. No. 2.4e-96;
1; Mismatches 4;
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Best Local Similarity 99.0%;
Matches 484; Conservative
                                                                                                                        VRETVGKLS 489
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158 BEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEA 217
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                                                                                                                                                                                                                                                            A;Cross-creferences: GB:AE004437; NID:g10581300; PIDN:AAG20060.1; GSPDB:GN00138 C;Genetics: A;Gene: htr3 C;Superfamily: Halobacterium salinarum transducer protein htrII
                                                                                                                                                                                                                                                                                                                                                   ---GDLTR-----RLDEDVDSEPM 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRG
                                                                                                                                                                                                                                                                                                                                                                                                                             QDIABAFNDMMG------AASTDVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 PLSSLEATSQDVAERTDTWRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 ALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 NORIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 IDDDTMAALAAEQPLFEATADALVTDFYDHLESYERT----QDLFANSTKTVEQLKETOA
                                                                                                                                                    24.9%; Score 597; DB 2; Length 63: 33.8%; Pred. No. 3e-19; ive 76; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-805 <KOK>
A;Cross-references: EMBL:AJ245950; PIDN:CAB82572.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 DRIATESQQVSAAAEEQAASVSEV 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: T48840
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                 Best Local Similarity 33.83
Matches 150; Conservative
      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-633 <STO>
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                                                                                                                                                                Query Match
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G.; Jablo
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C;Accession: T44973

R;Zhang, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.

Proc. Natl. Acad. Sci. U.S.A. 93, 4649-4654, 1996

A;Title: Signal transduction in the archaeon Halobacterium salinarium is processed throu A;Reference number: Z22804; MUID:96209786; PMID:8643458

A;Accession: T44973

A;Accession: T44973

A;Kesiques: preliminary; translated from GB/EMBL/DDBJ

A;Melecule type: DNA

A;Resiques: 1-482 < ZHA>
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G;Species: Halobacterium sp. NRC-1
G;Species: Halobacterium sp. NRC-1
G;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
G;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
G;Accession: H84336
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, I.Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl)
Jung, K.H.; Alam, M.; Freitas, T. 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; I.A.; I.Gerence anumber: A84160; MUID:20504483; PMID:11016950
A;Accession: H84336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 SVTSDVEALQNRIEDIDEVVDVITGIAEQTNMLALNASIEAAPPGEBGGFAVVAEEVKA 354
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                                                                                                                                                                                   A;Cross_references: EMBL:U75435; NID:g1654418; PIDN:AAB17880.1; PID:g1654419 A;Experimental source: strain Flx15 A;Note: the source is designated as Halobacterium salinarium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEDTLLDDEYIQIGRNLTEFGDTLAAHITEVHNDVERLEAASQAVSESSAEIDELSTAQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 LGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLL-----TFDQQI---
                                                                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                                  Length 482;
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                                                                                                                                                                                                                                                                    A,Gene: htpIII; htp3; htA
C,Superfamily: Halobacterium salinarum transducer protein car
C,Keywords: methylated amino acid; signal transduction
F;219-472/Region: MCP signalling domain similarity
                                                                                                                                                                                                                                                                                                                                                                25.5%; Score 609.5; DB 2;
llarity 37.2%; Pred. No. 6.2e-20;
Conservative 70; Mismatches 197;
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Best Local Simil
Matches 181; C
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transducer protein basT [validated] - Halobacterium salinarum N.Alternate names: chemotaxis transducer protein basT; methyl-accepting taxis protein ht C.Species: Halobacterium salinarum (C.Species: Halobacterium salinarum (C.Species: Nay-2000 #sequence_revision 05-May-2000 #text_change 02-Sep-2000 (C.Accession: T48840): T48840; T4881 (C.Accession: T48840): T48840; T4891 (C.Accession: T48840): T48760; T47656, 2000 Mol. Microbiol. 35, 647-656, 2000 A;Title: BasT, a membrane-bound transducer protein for amino acid detection in Halobacte A;Reference number: Z24542; MUID:20138366; PMID:10672186
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Proc. Natl. Acad. Sci. U.S.A. 93, 4649-4654, 1996
A,Title: Signal transduction in the archaeon Halobacterium salinarium is processed
A;Reference number: Z22804; MUID:96209786; PMID:8643458
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A;Experimental source: strain Flx15 derivative of S9
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162

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Hir4 transducer [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: F84237
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 1276-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
                         ---DLRRSFRDIQEYLQTVAGQADALAEQD 339
                                                                                                                                                                                                                                                                                                                   ----ATALNSLLEELEGTİHRIQRFSKDVAESSDHITTSA 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: GB:AE004437; NID:g10580376; PIDN:AAG19266.1; GSPDB:GN00138 C;Genetics:
A;Gene: htr4
C;Superfamily: Halobacterium salinarum transducer protein htrII
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                                                                   LFBATA------DALVTDFYD---HLESYERTQDLFANSTKTVEQLKETQAEYLLG
                                                                                                                                                                103 IGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA
                                                                                                                                                                                                                                                                163 AVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDBIDSRQELANAVA---THVEAPL
                                                                                                                                                                                                                                                                                                                                                                  220 SSLEATSQDVAERTDTWRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAE
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33.7%; Pred. No. 2.6e-18;
ive 75; Mismatches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     711 TTARAEDAAAABEQTASLTEVTNRIQDLS 740
                                                                                                                                                                                                                      -------AALESQAQDIRETVEHAAD---
                    286 MSDRAEAIAAGDIDTAIEETTRIDEVG-
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Best Local Similarity 33.7%
Matches 145; Conservative
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A, Molecule type: DNA
A, Residues: 1-778 <STO>
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B64236
Htr18 transducer [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Species: B64236
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-790 <STO>
A;Residues: 1-790 <STO>
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A;Residues: 1-70
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                                                                                       A Description: involved in chemotactic signal transduction; mediates the response C Superfamily: Halobacterium salinarum transducer protein htrII C Keywords: methylated amino acid; signal transduction; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVBA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EYSDEMAAAAA ------GDLTR------RLDEDVDSEPM 471
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larity 31.4%; Pred. No. 2.1e-18;
Conservative 84; Mismatches 190; Indels 76;
                                                                                                                                                                                                       DB 2; Length 805;
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                                                                                                                                                                                          24.9%; Score ..., 33.8%; Pred. No. 4e-19; rive 76; Mismatches 158; Indels
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C;Superfamily: Halobacterium salinarum transducer protein htrII
source is designated as Halobacterium salinarium
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Best Local Similarity
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...hes 150; Conservative
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Matches 160; Conserv
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C; Accession: T44849

R; Storch, K.F.; Rudolph, J.; Oesterhelt, D.

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R; Storch, K.F.; Rudolph, J.; Oesterhelt, D.

R; Storch, K.F.; Rudolph, J.; Oesterhelt, D.

R; Storch, K.F.; Rudolph, J.; Oesterhelt, D.

R; Status: Preliminary: Sensor responsible for arginine chemotaxis in the archaeon Hd

R; Reference number: 222859; MUID: 99164082; PMID: 10064582

R; Status: Preliminary; translated from GB/EMBL/DDBJ

R; Status: Preliminary; translated from GB/EMBL/DDBJ

R; Status: Preliminary; translated from GB/EMBL/DDBJ

R; Status: Preliminary; translated from GB/EMBL/DDBJ

R; Storchimental source: Strain S9

R; Note: the source is designated as Halobacterium salinarum

C; Genetics:

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N;Alternate names: arginine transducer protein Car; transducer protein htpl1;
C;Species: Halobacterium salinarum
A;Variety: strain S9
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000
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A;Reference number: Z24094; MUID:96275896; PMID:8674984
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Experimental source: strain S6
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                     RTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADD
                                                                                GEGFAVVADEVKALAEESREQSTRVEELVEOMQAETEETVDQLDEVNQRIGEGVERVEEA
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A, Accession: T48897
A, Accession: T48897
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-718 cMD-
A, Cross-references: EMBL: X95590; NID:g1435133; PIDN: CAA64843.1;
A, Experimental source: strain S6
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.larity 33.0%; Pred. No. 4.2e-18;
Conservative 74; Mismatches 168; Indels
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Transducer protein htpVI (similarity) - Halobacterium salinarum
NyAlternate names: methyl-accepting transducer protein htp; transducer protein htp6
Syspecies: Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000
C;Accession: T44597
Existang, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.
Proc. Natl. Acad. Sci. U.S.A. 93, 4649-4664, 1996
A;Title: Signal transduction in the archaeon Halobacterium salinarium is processed throu A;Reference number: Z22804; MUID:96209786; PMID:8643458
A;Accession: T44597
A;Accession: T44597
A;Accession: preliminary: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVE 406
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C;Superfamily: Halobacterium salinarum transducer protein htrII
C;Keywords: methylated amino acid; signal transduction; transmembrane protein
F;494-746/Region: MCP signalling domain similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U75438; NID:g1654424; PIDN:AAB17883.1; PID:g1654425
A;Experimental source: strain mFlx15
A;Note: the source is designated as Halobacterium salinarium
C;Genetics:
                                                                                                                                                                                                      84 NSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQR-----ARIGKIHDVLGLGPDVYLG
                                                                                                                                                                                                                                               346 NTAAAVQSLSAAAAE----IEAGNYDVDVASSRRDEIGQLFASİGSMRDALVTQIDEAEA
                                                                                                                                                                                                                                                                                              136 AYTRYYTGLLDALAD----DVVADRGEEAAAAVDELVA-----RFLPMLKLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGE
                                                                                                                                                                                                                                                                                                                                         402 AREQATEAQQDAEAERERAEDARERAEDAKADAEALAAELEAQAERYSDVMAACADGDLT
                                                                                                                                                                                                                                                                                                                                                                                     -----TFDQQIA--MDTYIDSYAQRLHDEIDSRQELANAVAT---HVEAPLSSLEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 777;
                                                                                                                           Length 810;
                                                                  Halobacterium salinarum transducer protein htrII
                                                                                                               23.1%; Score 554; DB 2; Length 81 ilarity 32.1%; Pred. No. 3e-17; Conservative 85; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 IADATDQQVRTVEEVRETVGKLS 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain S9
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                                                                                                          Query Match
Best Local Similarity
Matches 142; Conserv
A,Experimental source:
C,Genetics:
A,Gene: htpIV
C;Superfamily: Halobact
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Best Local Simil
Matches 141; C
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              C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
R;Accession: F843.7
R;NG; W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jroc, Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Recession: F84327
A;Retence number: A84160; MUID:20504483; PMID:11016950
A;Accession: F84327
A;Residues: 1-810 <STO>
A;Residues: 1-810 <STO>
A;Cross-references: GB:AE004437; NID:g10581215; PIDN:AAG19986.1; GSPDB:GN00138
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Tatein transducer protein IV (imported) - Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Becies: 17-Mar-2000 #text_change 02-Sep-2000
C;Accession: 146810
B;Rudolph, J; Nordmann, B.; Storch, K.F.; Gruenberg, H.; Rodewald, K.; Oesterhelt,
FEMS Microbiol. Lett. 139, 161-168, 1996
A;Title: A family of halobacterial transducer proteins.
A;Reference number: 24094; MUID:96275896; PMID:8674984
A;Accession: 146810
A;Accession: 146810
A;Accession: 146810
A;Accession: Paliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-810 &RUD>
A;Residues: 1-810 &RUD>
A;Cross-references: EMBL:X95589; NID:g1435131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.2%; Score 555; DB 2; Length 810; larity 32.1%; Pred. No. 2.7e-17; Conservative 85; Mismatches 174; Indels
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C,Superfamily: Halobacterium salinarum transducer protein htrII
       Halobacterium sp. NRC-1
NRC-1
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    [imported]
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Qy 249 DVSREISSVSASVEEVAASTADDVRRTSEDAEALAQQCEAAADDALATWTDIDEATDGVTA 308 1:	Oy 489 \$ 489 Db 500 \$ 500 RESULT 15 A84252 Htr15 transducer [imported] - Halobacterium sp. C; Species: Halobacterium sp. C; Species: Halobacterium sp. C; Species: Halobacterium sp. RC-1 C; Decise: Relb-2001 #sequence_revision 02-Feb-200 C; Accession: A84252 R; Mg, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquis, Leithauser, B.; Keller, K.; Cruz, R.; Danson, Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; A;Ttle: Genome sequence of Halobacterium specie A;Reference number: A84160; MUID:20504483; PMID; A;Retus: preliminary A;Molecule type: DNA A;Residues: 1-636 cSTO> A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics:	Query Match Best Local Similarity 29.7%; Pred. No. 1.5e-16; Matches 149; Conservative 99; Mismatches 191; Indels 63; Gaps 11; Matches 149; Conservative 99; Mismatches 191; Indels 63; Gaps 11; QY 17 IDGHALADRIGIDEAEIAWRISFIGIDDDTWAALAAEQPLEATADALVTD 67 16 VDDALLDSIGMEVFWLDATGSVVAWNETIEELTGCSKADAMGMDHASEA 214 OY 68 FYDHLESYERTODLFANSTKTVEQLKETQAEVLLGLGRGEYDTEYAAQRARIGKHUPUG 127
Qy 147 ALA	OY 347 RAGEAGEGRAVVADEVKALABESREGSTRVEELVEOWQAETEETVDOLDEVNORIGEGUE 406	A Molecule type: DNA A Molecule type: DNA A Molecule type: DNA A Secides: 1-534 <-SE1> A Recadeus: 1-534 <-SE1> A Recadeus: 1-534 <-SE1> A Recadeus: 1-534 <-SE1> A Recadeus: 1-534 <-SE1> A Recadeus: 1-534 <-SE1> A SEXPERIMENTAL SPI A Note: it is uncertain whether Met-1 or Met-22 is the initiator C Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics: A Genetics

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ALIGNMENTS

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RIR; E84304; E84304.

HSSP; P02942; 1QU7.

RINGEPTO; IPRO04089; Chmtaxis transd.

InterPro; IPRO04089; Me_chemotaxis.

R Pfam; PP00015; MCPsignal, 1.

R PRINTS; PR00250; CHEMTRNSDUCR.

R SMART; SM00283; MA; 1.

R PROSTTE; PS5011; CHEMOTAXIS_TRANSDUC_2; 1.

Transducer; Heme; Complete proteome.

T DOMAIN 218 454 METHYL-ACCEPTING TRANSDUCER.

SEQUENCE 489 AA; 52852 MW; 8COAEF179667791E CRC64;
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Pred. No. 3.9e-93;
1; Mismatches 4;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Halobacterial transducer protein III.
                  SUBUNIT: Homotetramer (Probable)
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W MGDINE=20504483; PubMed=11016950;
W MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorseon V., Sbrogna J.,
W Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo y.A.,
W Leithauser B., Keller K., Cruz R., Dannson M.J., Hough D.W.,
M Addocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
R Bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DassSarma S.,
T. "Genome sequence of Halbbacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
-!- FUNCTION: Heme-containing signal transducer responsible for
similarity).
                                                                                                                          ADALVĮDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG
                                                                                                                                                                                    1 MSNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEAT
                                                                                                                                                                                                                           KIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTF
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    METHYL-ACCEPTING TRANSDUCER.
8457263FCF616BFF CRC64;
                                                                                 Indels
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Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
                                                Score 2394; DB 1;
Pred. No. 1.4e-94;
0; Mismatches 0;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heme-based aerotactic transducer hemat.
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   454 ME
52816 MW;
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                                                100.0%;
100.0%;
                                                                           489; Conservative
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   218
489 AA;
                                                           Similarity
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               SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                    295 SVTSDVEALQNRIEDIDEVVDVITGIAEQTNMLALNASIEAARAGEEGEGFAVVAEEVKA 354
                                                                                                                                                                                                            415 TAEGIEQVSDATNEQAASAEEIAAAWDETADLADDITTAVADIVSQTEAQSAMLHDLDES 474
                                    GVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKA 364
                                                                                                                LAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVED 424
                                                                                                                                                                                      425 AASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRET 484
   235 TNVSTVATEVETLSATVQEIASTADEVVDTSATAERLADDGSAAASDAADMMADVATAAD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A family of halobacterial transducer proteins.",
FEMS Microbiol. Lett. 139:161-168(1996).
-!- FUNCTION: Potentially involved in chemo- or phototactic signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96275896; PubMed=8674984;
Rudolph J., Nordmann B., Storch K.F., Gruenberg H., Rodewald
Oesterhelt D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 481;
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METHYL-ACCEPTING TRANSDUCER.
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Halobacteríaceae; Halobacterium.
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28-FEB-2003 (Rel. 41, Last annotation update)
Halobacterial transducer protein III.
                                                                                                                                                                                                                                                                                                                                                                                                 481 AA
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PROSITE; PSS0112; PAS; 1.
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InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004090; Me_chemotaxis.
InterPro; IPR000014; PAS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00015; MCPaignal; 1.
PRINTS; PR0260; CHEMTRNSDUCR.
SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
SMART; SM00281; PAS; 1.
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Q48316;
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MEDIANE-20504483; PubMed=11016950;
MEDIANE-20504483; PubMed=11016950;
MEDIANE-20504483; PubMed=11016950;
MEDIANE-1 Lasky S.P., Mahairas G.G., Berquist B., Pan M.,
Ankla H.D., Lasky S.P., Baliga N.S., Thorsson V., Sbrogna J.,
Aswartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Alam M., Freitas T., Hou S., Danisch M.P., Angerine C.M., Dan B.
Alam M., Freitas T., Hou S., Danisch S., Dennis P.P., Omer A.D.,
Abardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Genome sequence of Halobacterium species NRC-1 ";
From Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
C. -- FUNCTION: Potentially involved in chemo- or phototractic signal transduction (By similarity).
C. -- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
C. -- SIMELARITY: Contains I methyl-accepting transducer domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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           Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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SMART; SMO0304; HAMP; 1.
SMART; SMO0281; MA; 1.
SMART; SMO0091; PAS; 1.
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
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InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
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InterPro; IPR000014; PAS domain.
Pfam; PF00015; MCPsignal; 1.
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(Rel. 37, Created)
(Rel. 37, Last sequence update)
                                                                                                                                                                  InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004089; HAMP.
InterPro; IPR004090; Me_Chemotaxis.
Ffam; PF00672; HAMP; 1.
Pfam; PF00615; MCPsignal; 1.
Pfam; PR00260; CHEMTRNSDUCR.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                  EMBL; AE005022; AAG19266.1; -.
                                                                                                                                                                                                                                                                                                                                                                  Transducer; Transmembrane;
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738 AEQATTLSDV 747
                                                                                                                                    PIR; F84237; F84237.
HSSP; P02942; 1QU7.
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15-DEC-1998
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MEDLINE-2004483; PubMed=11016950;
MEDLINE-2004483; PubMed=11016950;
MA SHUKIR-2004483; PubMed=11016950;
MA SHUKIR H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
SWATZZELL S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.B., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
R. Mann M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
R. Genome sequence of Halobacterium species NRC-1 ",
Perox. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
C. -I- FUNCTION: Potentially involved in chemo- or phototactic signal
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                                                                                                                                    74 SYERTODLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAEESREQSTRVEELVEOMOAETERTVDQLDEVNQRIGEGVERVEEAMETLQEITDAVED 424
                                                           73
                                                                                                 63
                                                                                                 19 NTLDVPAFA--VDADGAVVAW-----DDQIAAL----LETAPEDAIGVTDIGERLN
                                                                                                                                                                        64 D----DGSRALANKVADTPIDAHHEY---DGVGLADESYALLTGDYVYEDTTVAGNTDLW
                                                                                                                                                                                                             134 LGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLL-----TFDQQI---
                                                                                                                                                                                                                                                                                                            <u>AASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRET</u>
                                                           15 NGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATADAL-VTDFYDHLE
                                                                                                                                                                                                                                                                                                                                                                DRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATD
                                                                                                                                                                                                                                                                                       185 AMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQV
                     Gaps
                       34;
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-!- SIMILARITY: Contains 2 HAMP domains.
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Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                     Indels
37.6%; Pred. No. ....
rive 72; Mismatches 196;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HTR4 OR HTPVI OR VNGO806G.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PSS0885; HAMP; 2.
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PIR; F84327; F84327.
HSSP; P02942; 10U7.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
Pfam; PF00672; HAMP; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
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323
344
810
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Halobacterium sp.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=64091;
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16-0CT-2001
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Q9HP84;
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                                                                                                                                                          FEMS Microbiol. Lett. 139:161-168 (1996).
-!- FUNCTION: Potentially involved in chemo- or phototactic signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                             -!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
-!- SIMILARITY: Contains 2 HAMP domains.
                                                                                                              MEDLINE=96275896; PubMed=8674984;
Rudolph J., Nordmann B., Storch K.F., Gruenberg H., Rodewald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 573; DB 1; Length 778; Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYL-ACCEPTING TRANSDUCER.
134C7D7F0A3334CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                           Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                              "A family of halobacterial transducer proteins.";
                                                                                                                                                                                                                                                                                                                                           HSSP; P02942; 1007.
InterPro; IPR004689; Thamp:
InterPro; IPR004689; HAMP.
InterPro; IPR004080; Me_chemotaxis.
Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPsignal; 1.
PRINTS; PR00260; CHEMTRNSDUCR.
SMART; SM00283; MAP; 2.
SMART; PS0011; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
28-FEB-2003 (Rel. 41, Last annotation update)
Halobacterial transducer protein VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMP 1.
HAMP 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transducer; Transmembrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82077 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.9%;
33.0%;
                                                                                                                                                                                                                                                                                                                        EMBL; X95590; CAA64843.1; -. PIR; T48897; T48897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                  Halobacterium salinarium.
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                                                                                        SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=2242;
                                                                                                                           Rudolph J., No:
Oesterhelt D.;
                       HTR4 OR HTPVI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Sim
Matches 144;
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TRANSMEM
DOMAIN
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                                                                                                                                  405
                                                                                                                                                                                                                                                                                                  ERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALD 465
                                                                                                                                                                                                                                                                                                                                                               ETVSETERSLSEIAGRIAEADIGVQEISNAMDDQAASVSDVTTAVGDVAALGEETATEAE 731
MEDLINE=20504483; PubMed=11016950;
A Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Leithauser B., Weiler K., Cruz R., Danson M.J., Hough D.W.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
A maddocks D.G., Jablonski P.B., Krebs M.P., Angevine C.M., Dale H.,
A lam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A behardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
T. "Genome sequence of Halbbacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000)
-!- FUNCTION: Potentially involved in chemo- or phototactic signal transduction (By similarity).
-!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
                                                                                                                                                                             ARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (strain NRC-1 / ATCC 700922 / JCM 11081).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
12-FBD-acterial transducer protein IV.
HTRS OR HTPIV OR VNG1760G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 810 AA.
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PROSITE; PS50885; HAMP; 2.
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85; Mismatches 174; Indels
                                                                                                                                                                                                                                                                          METHYL-ACCEPTING TRANSDUCER
                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                       85207 MW; 37B0F6046A39D9BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natronomonas pharaonis (Natronobacterium pharaonis).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                               23.1%; Score 554; DB 1; 32.1%; Pred. No. 8.3e-17;
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                                                                                     Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
PROSITE; PSS0111; CHEMPTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 2.
 an email to license@isb-sib.ch)
                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                         POTENTIAL
                                                 HSSP; P02942; 1QU7.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 IADATDQQVRTVEEVRETVGKLS
                                                                                                                                                                      Transducer; Transmembrane;
                           EMBL; X95589; CAA64841.1;
                                                                                                                                                                                                                                                                                                                             Best Local Similarity 32.1
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                      T46810; T46810.
                                                                                                                                                                                                                                                                                       810 AA;
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345
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512
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                                                                                                                                401
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                                                                                                                       402 AREQATEAQQDAEAERERAEDARERAEDAKADAEALAAELEAQAERYSDVMAACADGDLT
                                                                                                                                                                                                                           287 AAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAA
                                                                                                                                                                                                                                                                                                                                 407 RVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDD
                                                                                                                                                                                                          -----TFDQQIA--MDTYIDSYAQRLHDEIDSRQELANAVAT---HVEAPLSSLEATS
                                                                                                                                                                                                                                                           227 QDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGE
                                                                                                                                                                                                                                                                             136 AYTRYYTGLLDALAD----DVVADRGEEAAAAVDELVA-----RFLPMLKLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A family of halobacterial transducer proteins.";
FEMS Microbiol. Lett. 139:161-168(1996).
-!- FUNCTION: Potentially involved in chemo- or phototactic signal
transduction.
                                                                             42;

    -!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
    -!- SIMILARITY: Contains 2 HAMP domains.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodewald
                                                     Length 810;
            748 METHYL-ACCEPTING TRANSDUCER.
B5219 MW; 4BF36E4B7D22BD80 CRC64;
                                                                            85; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
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Rudolph J., Nordmann B., Storch K.F., Gruenberg H.,
Oesterhelt D.;
                                                   23.2%; Score 555; DB 1; 32.1%; Pred. No. 7.5e-17;
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
HTRS OR HTPIV.
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                                                                             Conservative
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439 4
512 7
810 AA;
                                                                Similarity
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                                               Query Match
Best Local Simi
Matches 142;
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             DOMAIN
SEQUENCE
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                                                                                                                            | : : : : | | : : 402 AREQATEAQODAEAERERAEDAKADAEALAAELEAQAERYSDVMAACADGDLT 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2004 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis
protein II) (MPP-II).
                                                                                                                                                                                                                                                                                                                      347 RAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVE
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                                                                                                                                                                                                                                                                                                                                                                                           227 QDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGE
                                                                                                                                                                                            136 AYTRYYTGLLDALAD----DVVADRGEBAAAAVDELVA-----RFLPMLKLL-
                                                42;
Length 810;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GINLGLVAATLGGDTAASLSTLAAKASRMG-DGDLDVEL-----ETRREDEIGDLYAA
                                                                                                                                                                                                                                                                                                                        FUNCTION: Transduces signals from the phototaxis receptor sensory rhodopsin II (SR-II) to the flagellar motor. Responds to light changes through the variation of the level of methylation. Also acts as a chemotransducer.
                                                                                                                                                                                                                              Gordeliy V.I., Labahn J., Moukhametzianov R., Efremov R., Granzin J.,
Schlesinger R., Bueldt G., Savopol T., Scheidig A.J., Klare J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pfam; PF00672; HAMP; 1.
PFAM; PF00615; McPsignal; 1.
PR MORS PF00015; McPsignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
PROSTIE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSTIE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSTIE; PS50101; CHEMOTAXIS_TRANSDUC_2; Transducer; Photoreceptor; Chemotaxis; Transmembrane; Methylation;
                                                                                                                                                                                                                                                                            "Molecular basis of transmembrane signalling by sensory rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                           an
                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Contains 1 methyl-accepting transducer domain.
SIMILARITY: Contains 2 HAMP domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.5%; Score 537.5; DB 1; Length 534; 31.2%; Pred. No. 2.6e-16;
                                                                                                                      "The primary structure of sensory rhodopsin II: a member of additional retinal protein subgroup is coexpressed with its transducer, the halobacterial transducer of rhodopsin II."; Proc. Natl. Acad. Sci. U.S.A. 92:3036-3040(1995).
                                                                                Seidel R., Scharf B., Gautel M., Kleine K., Oesterhelt D.,
Engelhard M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHYL-ACCEPTING TRANSDUCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBE8012CC5F278E8 CRC64;
                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 23-82.
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EXTRACELLULAR
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InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
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HAMP 2.
                                                           STRAIN-SP-1 / 28;
MEDLINE-95224074; PubMed=7708770;
   Halobacteriaceae; Natronomonas.
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                                                                                                                                                                                                                                                                                         II-transducer complex.";
Nature 419:484-487(2002).
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43
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534
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DOMAIN 1
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                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                 PubMed=12368857;
                NCBI_TaxID=2257;
                                                                                                                                                                                                                                                              Engelhard M.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
129 GPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDT 188
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MEDLINE=20504483; PubMed=11016950;

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Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

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Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

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                                                                                                                                                                                              189 YIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMA
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FEMS Microbiol. Lett. 139:161-168(1996).
-!- FUNCTION: Potentially involved in chemo- or phototactic signal
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MEDLINE=96275896; PubMed=8674984;
Rudolph J., Nordmann B., Storch K.F., Gruenberg H., Rodewald K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and
Halobacterium salinarium.
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Halobacteriaceae, Halobacterium.
NCPI_TaxID=64091, 2242;
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protein II) (MPP-II) (Fragment).
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P42258;
01-NOV-1955 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis
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29.6%; Pred. No. 1.3e-15;
ive 94; Mismatches 195; Indels
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InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
InterPro; IPR003609; Me chemotaxis.
Pfam; PF000115; MCPSignal; 1.
PRINTS; RN00260; CHEMTRNSDUCR.
SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
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TRANSMEM 10 30 POTENTIAL.
                                                 send an email to license@isb-sib.ch).
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                                                                       EMBL; AE005080; AAG19985.1; -. EMBL; X95589; CAA64842.1; -. PIR; E84327; E84327. PIR; T46811. HSSP; P02942; IQU7.
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Best Local Similarity 29.64
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 GPDVYLGAYTRYYTGLLDALADD-----VVADRGEEAAAAVDELVARFLPMLKLLTFDQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 IAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 NEGLESAAAEMONLSATAQOVASSAQOVADTSOSAAKVGEDGREAAQEA1AEMSAIEAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                               "The primary structure of sensory rhodopsin II: a member of an additional retinal protein subgroup is coexpressed with its transducer, the halobacterial transducer of rhodopsin II."; Proc. Natl. Acad. Sci. U.S.A. 92:3036-3040(1995).

-!- FUNCTION: Transduces signals from the phototaxis receptor sensor rhodopsin II (SR-II) to the flagellar motor. Responds to light changes through the variation of the level of methylation. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acts as a chemotransducer.
SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
SIMILARITY: Contains 1 methyl-accepting transducer domain.
SIMILARITY: Contains 1 HAMP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transducer; Photoreceptor; Chemotaxis; Transmembrane; Methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 433;
                                                                                                                                                                                                                   STRAIN=ATCC 29715;
MEDLINE=95224074; PubMed=7708770;
Seidel R., Scharf B., Gautel M., Kleine K., Oesterhelt D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 366 METHYL-ACCEPTING TRANSDUCER
433 AA; 45935 MW; 90507BB897D943C0 CRC64;
                                       Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.6%; Score 492; DB 1; 29.9%; Pred. No. 1.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1. PROSITE; PS50885; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004089; Chmtaxis_transd.
InterPro; IRR00360; HAMP.
InterPro; IRR004090; Me chemotaxis.
Pfam; PF00015; MCP8ignal; 1.
PRINTS; PR00260; CHEMTRNSDUCR.
SMART; SM00104; HAMP; 1.
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                                                                           Halobacteriaceae; Haloarcula
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Haloarcula vallismortis
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                                                                                                                                                                               SEQUENCE FROM N.A.
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Engelhard M.;
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AN WOLLINE=20504483; PubMed=11016950;

AN WOLLINE=20504483; PubMed=11016950;

AN WOLLINE=20504483; PubMed=11016950;

AN Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

AN Swartzell S., Weir D., Hall J.L., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

AN Maddocks D.G., Jabhonski P.E., Krebs M.P., Angevine C.M., Dale H.,

AN Bandacks D.G., Jabhonski P.E., Krebs M.P., Angevine C.M., Dale H.,

A Liembarger T.A., Peck R.F., Pohlschroder M. Spudich J.L., Jung K.-H.,

A Lischarger T.M., Liang P., Riley M., Hood D., DasSarma S.,

A Ebhardt H., Lowe T.W., Liang P., Riley M., Hood L., DasSarma S.,

A Ebhardt H., Lowe T.W., Liang P., Riley M., Hood L., DasSarma S.,

B. Choome sequence of Halobacterium species NRC-1.",

Broc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

C. Fronchopsin II (SR-II) to the flagellar motor. Responds to light changes through the variation of the level of methylation. Also

C. I- SUMLARITY: Contains 1 methyl-accepting transducer domain.

C. I- SIMILARITY: Contains 2 HAMP domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
364 ALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVE 423
                                   276 GLAEETKEAAADIEGRIEAIQEQAGDTVETMESTSTRITEGVSTVEETVDALETIVEYTE 335
                                                                                                             424 DAASGMOEVSTATDEGAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDOGVRTVEEVRE 483
                                                                                                                                              15-WAR-2004 (Rel. 43, Last annotation update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis
protein II) (MPP-II).
HTR2 OR VNG1765G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemotaxis; Transmembrane; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                   763 AA
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Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
PROSITE; PS50111; CHEMOTAXIS TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 2.
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Last sequence update)
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InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 LVEÇMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDE 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 LSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQ
                                                                                                                                                                                                                                                                                                                                                                                                                             293 LSLIGVTVGSTTVTALRO--FSRRADEMAAGDLDTDIDTSR-NDEFGTLAESFRSMRDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 AEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 SESLT------DAERATARAEDAR-EDAEQQRADA-------EAAREDAEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 --GEEAAAAVDELVARFLPMLKLLT---FDQQIAMDTYIDSYAQRLH-----DEIDSRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 ELANAVATHVEAPLSSLEA-----TSQDVAERTDTMRARTDDQVDRMADVSREISSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 ASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMIDIDEAIDGVTAGVEQLGERAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629 RILALÓGOVSDVADEMRATSDTVSDGRATVGDÁATALDDVVSFVADTDTAAGEIRAATDR
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                   42;
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                                                                                                                                                                                                                                  Length 763;
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                                                                                                                                    METHYL-ACCEPTING TRANSDUCER.
                                                                                                                                                                                                                                                                                                   Indels
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Halobacterium halobium.
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091, 2242;
                                                                                                                                                                     CF7A8FF04DFF309A CRC64;
                       CYTOPLASMIC (POTENTIAL) HAMP 1.
                                                                                                                                                                                                                                                                 Pred. No. 4.8e-13; 74; Mismatches 219;
                                                                                                                                                                                                                                      Score 464;
          POTENTIAL.
                                                                                                     HAMP 2
297 PO
763 CY
354 HA
449 HA
704 ME
                                                                                                                                                                                                                                  19.48;
                                                                                                                                                                                                                                                                 28.9%;
                                                                                                                                                                                                                                                                                         136; Conservative
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                                                                                                                             468 763 AA;
                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                             345 IEAARAGGNADGDGFSVVADEVKDLAEETQDRANEIAAVVEKVTAQTEDVTASIQQTRTR 404
----LTQRVDVDTDHEAMETVGTAFNQMMDDLQATVRTVTTVADEIEAKTERMSETSADI 224
                                                           230 -AERTDIMRA-----RIDDQVDRMADVSREISSVSASVEEVASTADDVRRISEDAEALA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                               401 IGEGVERVEEAMETLOEITDAVEDAASGMOEVSTATDEQ-----AVSTEEVAEMVD-- 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 VESGSETVESTLRDIRTIADSIAEVSNSIDEIQRTTSEQAETVQSTATSVERVAGLSDDT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis protein II) (MPP-II).
                                                                                                   225 EASAGDIVEAVSKIESQANDQRTELDSAADDVQQVSASAEEIAATIDDLASRSEDVATAS
                                                                                                                                                                                                                                 Zhang W., Brooun A., Mueller M.M., Alam M.;
"The primary structures of the Archaeon Halobacterium salinarium blue
light receptor sensory rhodopsin II and its transducer, a methyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hou S., Brooun A., Yu H.S., Freitas T., Alam M.;
"Sensory rhodopsin II transducer HtrII is also responsible for serine chemotaxis in the archaeon Halobacterium salinarum.";
J. Bacteriol. 180:1600:1602(1998).
-:-FUNCTION: Transduces signals from the phototaxis receptor sensory rhodopsin II (SR-II) to the flagellar motor. Responds to light changes through the variation of the level of methylation. Also
                                                                                                                                                                                      283 QQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNAS
                                                                                                                                                                                                                                                                                                                    343 IEAARAG--EAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity). -!- SIMILARITY: Contains 1 methyl-accepting transducer domain. -!- SIMILARITY: Contains 2 HAMP domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GVDDRAGEIAAALDDIADATDQQVRT-----VEEVRETVG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 TALASDAESAVIGQRESAEEIAASLEQFQNTAVEQLQSRVASFTVATEDSETAG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea, Euryarchaeota, Halobacteria, Halobacteriales;
Halobacteriaceae, Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 93:8230-8235(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         764 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004089; Chmtaxis transd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96323203; PubMed=8710852;
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PIR; T44946; T44946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halobacterium salinarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 accepting protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 TNDVPSTIVA----GIAG--LLTLGSINAAETVASIKEIAAQTERVANGNLEQEVTSTRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 RIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGE--EAAAAVDELVARFLPML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7 QAAERE------ARELAATYQDTAKRYGETMEAAATGD------
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                                                                                                                                                                                   methyl-accepting protein associated with sensory rhodopsin I.";
Proc. Natl. Acad. Sci. U.S.A. 89:11915-11919 (1992).
-!- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTRXIS RECEPTOR
SENSORY RHODOPSIN I (SR-I) TO THE PLAGELLAR MOTOR. RESPONDS TO
-!- LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.
-!- SIMILARITY: CONtains 1 methyl-accepting transducer domain.
-!- SIMILARITY: Contains 2 HAMP domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95;
                             SEQUENCE FROM N.A., AND SEQUENCE OF 1-10; 350-377 AND 457-476. SPECIES=H.halobium; STRAIN=FLKSR; MEDLINE=93101637; PubMed=1465418; Yao V.J., Spudich J.L.; All J.L.; All J.L.; Spudich J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L.; All J.L
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B9945E4F66A9D091 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.4%; Score 463.5; DB 1 27.5%; Pred. No. 3.5e-13;
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PROSITE; PSS0885; HAMP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHYLATION
METHYLATION
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PIR; E84318; E84318.
HSSP; P02942; 1007.
InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR003660; HAMP.
InterPro; IPR003660; Me_chemotaxis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCBaignal; 1.
PRINTS; PR00260; CHEMTRNSDUCR.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
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Best Local Similarity 27.5
Matches 147; Conservative
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01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Sensory rhodopsin I transducer (HTR-I) (Methyl-accepting phototaxis
                                                              Transducer; Photoreceptor; Chemotaxis; Transmembrane; Methylation;
                                                                                                                                                                                                          42;
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                                                                                                                                                                                     Score 461; DB 1; Length 764;
Pred. No. 6.4e-13;
75; Mismatches 219; Indels
                                                                                                                                                          METHYL-ACCEPTING TRANSDUCER.
                                                                                                    POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                    1E0D7B4E460FC588 CRC64;
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Halobacteriaceae; Halobacterium.
                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                               SESLT-----DAERATARAEDAR-EDAEQQRADA---
       Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPsignal; 1.
SMART; SMO304; HAMP; 2.
SMART; SM00283; MA; 1.
PROSITE; PS50111; CHEWOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 2.
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                                                                                  SIMILARITY
                                                                                                                       POTENTIAL.
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InterPro; IPR003660; HAMP.
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HTRI OR HTRI OR HTR.
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[1] SEQUENCE FROM N.A.

NCBI_TaxID=2242;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 LLDALADDVVADRGE--EAAAAVDELVARFLPMLKLLTFDQQI-----AMDTYIDSYA 194
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MEDLINE=90384855; PubMed=2205842;
Ferrando E., Krah M., Marwan W., Oesterhelt D.;
"A gene from S. pombe with homology to E. coli RNase III blocks
conjugation and sporulation when overexpressed in wild type cells.";
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                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSORY RHODOPSIN I (SR-1) TO THE FLAGELLAR MOTOR. RESPONDS TO LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION. -!- SIMILARITY: CONtains 1 methyl-accepting transducer domain. -!- SIMILARITY: Contains 2 HAMP domains.
                                                                                                                                                                                       MEDLINE=94244615; PubMed=8187768;
Krah M., Marwan W., Vermeglio A., Oesterhelt D.;
"Phototaxis of Halobacterium salinarium requires a signalling coi
of sensory rhodopsin I and its methyl-accepting transducer HtrI.'
EMBO J. 13:2150-2155(1994).
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SMART; SMOO304; HAMP; 2.

SMART; SMOO304; MA; T.

PROSITE; PSSO111; CHEMOTAXIS_TRANSDUC_2; 1.

PROSITE; PSSO885; HAMP; 2.

Transducer; Photoreceptor; Transmembrane; Methylation; Repeat.

INT_MET 0

BX SIMILARITY.
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InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
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Search completed: August 10, 2004, 15:26:49 Job time : 16.3923 secs Н Page

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 10, 2004, 15:22:05; Search time 58.609 Seconds (without alignments) 2632.505 Million cell updates/sec Run on:

US-09-455-978B-2 2394

1 MSNDNDTLVTADVRNGIDGH........ATDQQVRTVEEVRETVGKLS 489 Perfect score:

BLOSUM62 Scoring table: Sequence:

1017041 seqs, 315518202 residues Searched:

Gapop 10.0 , Gapext 0.5

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL 25:* Database

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_organele:*
sp_organele:*
sp_phage:* unclassified:* sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_plant:*
sp_rodent:*
sp_virus:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

O9hp10 halobacteri O9p9j0 halobacteri Oghr88 halobacteri O93775 halobacteri P71415 halobacteri P71412 halobacteri P71414 halobacteri Description P71412 Q9P910 Q9P910 Q9PR88 C93775 P71414 Q9HQX8 P71414 Q9HQX8 Q9HQS Q9HPQS Q9HPQS Query Match Length DB 633 805 790 7790 7790 7792 636 804 804 7389 7388 7388 Score Result No.

Q9hqx8 halobacteri P71416 halobacteri O06022 halobacteri

Q9hpq5 halobacteri Q9hrn6 halobacteri Q9hra1 halobacteri 093643 halobacteri Q9hpw6 halobacteri

093643 09HPW6

P71409 halobacteri

059634 halobacteri Q9uxs0 haloarcula Q9hs86 halobacteri	093644 halobacteri Q9hpa2 halobacteri Q9ab06 caulobacter	- 4	Q815u4 bacillus ce Q9k669 bacillus ha	Q88117 pseudomonas O9a5v0 caulobacter			Osuqlo agrobacteri		O32440 pseudomonas	Q8d3w6 vibrio vuln	Q87qg4 vibrio para		Q9XUm/ thermotoga Oshwal pesudomonas			Q9iOr3 pseudomonas	Q81xf7 bacillus an	Q97d01 clostridium	Q8d3r3 vibrio vuln
1 059634 1 09UXS0 17 09HS86	0 7 9	O		16 Q88L17 16 Q9A5Y0		16 Q8P6P5		16 Q9K632	0				16 Q9AUM/	_	9		9		16 Q8D3R3
642 773 627		423					499		•	•		678 1				535		21	623
	000	18.9	17.5	17.4	17.3	17.1	17.0	16.9	16.9	16.9	16.8	16.8	16.8		16.7	16.7	16.7	16.7	16.6
502 502.5 499.5	497.5 497 475.5	452.5		415.5	413	410.5	408	405.5	405.5	405	403	403	401	400.5	400	99		399	398
17 18 19	27 27 27 27	24.3	25 26	27	29	30	32	33	34	35	36	37	3 6	40	41	42	43	44	45

ALIGNMENTS

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Halobacterium salinarum.
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                            GO: GO: 0016020; C: membrane; IEA.
GO: GO: 0004871; F: signal transducer activity; IEA.
GO: GO: 0006335; P: signal transducer activity; IEA.
GO: GO: 0007165; P: signal transduction; IEA.
InterPro: IPR004089; Chmtaxis_transd.
InterPro: IPR004089; Chmtaxis_transd.
InterPro: IPR004099; Map.
InterPro: IPR004099; Map.
InterPro: IPR004001; PAS domain.
Pfam: PF00015; PR005001; PAS domain.
Pfam: PF00015; PR00500; CHEMTRNSDUCR.
SMART; SM00283; MAP: 1.
SMART; SM00283; MAP: 1.
SMART; SM00281; PAS; 1.
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
                                                      02, Last sequence update)
24, Last annotation update)
                       482 AA
                                            Created)
                      PRT;
                                           02,
02,
                    PRELIMINARY;
                                         01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                          Transducer HtA protein.
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=2242;
                               P71412;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 LDEDLPGAFGASLSOMHTRLEALITDLDEAREDAEQTRKDAEEARAASERLNERLERRAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 SAAEIRSASDQVSESVQDISADADQQRDRLGTVGDEVTSLSATVEEIAASADDVAETVNQ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 AEALAQQGEAAADDALATMIDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNML 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 ALNASIRAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 NQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20138366; PubMed=10672186; Kokoeva M.V., Oesterhelt D.; "BasT, a membrane-bound transducer protein for amino acid detection in "BasT, a membrane-bound transducer protein for amino acid detection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 PLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

24.9%; Score 597; DB 17; Length 6
Best Local Similarity 33.8%; Pred. No. 5.7e-18;
Matches 150; Conservative 76; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4D8022B66ECD0FF CRC64;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006935; P:signal transduction; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004090; Me_Chemotaxis.
Pfam; PF00015; HAMP; 1.
Pfam; PF00015; MCP8ignal; 1.
PRINTS; PR00206; CHEMPTRNSDUCR.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
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Last annotation update)
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PROSITE; PS50885; HAMP; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577 DRIATESQQVSAAAEEQAASVSEV 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633 AA; 66423 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 633 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 GVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --DAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADDQVRTVEEV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 DRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATD 304
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                                                                                                                                                                                                                                                 15 NGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADAL-VTDFYDHLE
                                                                                                                                                                                                                                                                                       74 SYERTODLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 LGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLL-----TFDQQI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 AMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 TNVSTVATEVETLSATVQEIASTADEVVDTSATAERLADDGSAAASDAADMMADVATAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 TAERASNM--VSDATNEQAASAEEIAAMVDETADLADDITTAVADIVSQTEAQSAMLHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                              64 D----DGSRALANKVADTPIDAHHEY---DGVGLADESYALLTGDYVYEDTTVAGNTDLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 AEDILLDDEYIQIGRNLTEFGDILAAHITEVHNDVERLEAASQAVSESSAEIDELSTAQS
                                                                                                                                                                                  Gaps
                                                                                                                                                                              39;
                                                                                                            DB 1; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea, Buryarchaeota, Halobacteria; Halobacteriales;
Halobacteriaceae, Halobacterium.
                                      50872 MW; ECBEF79B3374CEC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                           70; Mismatches 197;
                                                                                                                                        2e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   633 AA.
                                                                                                        25.5%; Score 609.5; 37.2%; Pred. No. 1.2
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PIR; H84336; H84336.
HSSP; P02942; 1QU7.
                                                                                                                                               Best Local Similarity 5..2.
Matches 181; Conservative
             PROSITE; PS50112; PAS; 1.
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                                                                                                                                           Local Similarity
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                                      SEQUENCE
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385 LDEDLPGAFGASLSQMHTRLEALITDLDEAREDAEQTRKDAEEARAASERINERLERRAA
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                                                                                                                                                                                                                                           42 IDDDIMAALAAEQPLFEATADALVTDFYDHLESYERT----QDLFANSTKTVEQLKETQA
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
HINB transducer.
HTR18 OR VNG0812G.
HARDAGACTETIUM Sp. (Strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarcheeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                      24.9%; Score 597; DB 1; Length 805; 33.8%; Pred. No. 7.6e-18; ive 76; Mismatches 158; Indels
                                                                                                                                                                                     805 AA; 84831 MW; 089CA734D3F9DE3D CRC64;
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                                                                                                                                                              PROSITE; PS50111; CHEWOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 2.
SEQUENCE 805 AA; 84831 MW; 089CA734D3F91
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SEQUENCE FROM N.A
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01-MAR-2001
01-MAR-2001
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MEDLINE=20504483; PubMed=11016950;

Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

EMBL, AE005023; AAG19270.1; -
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0006931; F:sapmal transducer activity; IEA.

GO; GO:0006935; P:chemotaxis; IEA.

GO; GO:0007165; P:sapmal transduction, IEA.

InterPro; IPR004089; Chmtaxis_transd.

InterPro; IPR004089; Chmtaxis_transd.

InterPro; IPR004089; Chmtaxis_transd.

R InterPro; IPR004089; Chmtaxis_transd.

R Pfam; PF00015; MCPEignal; 1.

R Pfam; PF00015; MCPEignal; 1.

R Pfam; PF00015; MCPEignal; 1.

R SMART; SM00304; HAMP; 2.

R SMART; SM00304; HAMP; 2.
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24.2%; Score 580; DB 17; 1
Best Local Similarity 31.4%; Pred. No. 3.9e-17;
Matches 160; Conservative 84; Mismatches 190;
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PROSITE; PS50885; HAMP; 2.
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MEDLINE=99164082; PubMed=10064582;
Stock K.F., Rudolph J., Oesterhelt D.;
Car: A cytoplasmic sensor responsible for arginine chemotaxis in the archaeon Halobacterium salinarum.";
EMBO J. 18:1146-1158(1999).
EMBL, AJ132221; CAB38318.1; -.
PIR; T44849; T44849.
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0004871; F:signal transducer activity; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro: IPR004099; Me chemotraxis.

R InterPro: IPR004099; Me chemotraxis.

R InterPro: IPR00014; PAS_domain.

R FAM: PP00015; MCP84gnal; 1.

R PRINTS; PR00260; CHEMTRNSDUCR.

SMART; SM0028; MA; 1.

R SMART; SM00021; PAS; 1.

TIGRFAMS; TIGR00229; Sensory_box; 1.

PROSITE; PSSO111; CHEMOTAXIS TRANSDUC 2; 1.

SRQUENCE 452 AA; 49098 MW; 9244D900D694681A CRC64;
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                                                                                                                                                                                                                                   Halobacterium salinarum.
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
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                                                                                                   Last sequence update)
Last annotation update)
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                                                                      Created)
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PRELIMINARY;
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Matches 159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                            01-MAY-1999 (
01-MAY-1999 (
01-JUN-2003 (
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MEDLINE=96209786; PubMed=8643458;
Zhang W., Brooun A., McCandless J., Banda P., Alam M.;
Kignal transduction in the archaeon Halobacterium salinarium is
processed through three subfamilies of 13 soluble and membrane-bound
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Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006935; P:chemctaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004099; Chutaxis_transd.
InterPro; IPR004099; Chutaxis_transd.
InterPro; IPR004099; Me_chemctaxis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transducer proteins.";
Proc. Natl. Acad. Sci. U.S.A. 93:4649-4654(1996).
EMBL; U75438; AAB17883.1; -.
PIR; T44597; T44597.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00672; HAMP; 1.
Pfam; PF0015; MCPSignal; 1.
PRINTS; PR00260; CHEMIRNSDUCR.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
                                                                                                                                                                          777 AA
423 EDRLDNLSQIASEQHDRVAEIEDMVDEL 450
                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 141; Conservative
                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                               Halobacterium salinarum
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398 NORIGEGVERVEEAMETLOEITDAVEDAASGMOEVSTAIDEQAVSTEEVAEMVDGVDDRA 457
                  556 AATESERGQELGEDAVAELERIEATADSAVERVTALEEAVDAIGHVTGVITDIAEQTNML 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 FYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLG 127
                                                                                                                                                                                                                                    MEDLINE-20504483; PubMed=11016950; Mariate B., Pan M., Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shronady S.P., Mahairas G.G., Berquist B., Pan M., Shronady S.P., Malaiga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keiler K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.P., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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HSSP; P02942; LQU7.

HSSP; P02942; LQU7.

HSSP; P02942; LQU7.

HSSP; P02942; LQU7.

HSSP; P02942; LQU7.

HSSP; P02942; LQU7.

HSSP; P02942; LQU7.

HSSP; P00101650; Cimedrane; IEA.

HSSP; P00100160; P: Temo-component sensor molecule activity; IEA.

HSSP; P00100160; P: Temo-component signal transduction system (p. InterPro; IPR004009; Chmtaxis transd.

InterPro; IPR004009; Chmtaxis transd.

InterPro; IPR0000010; PAS-assoc_C.

InterPro; IPR0000014; PAS-domain.

Pfam; PF00015; MCPsignal; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                          736 DRTATESQOVSAAAEEQAASVSEV 759
                                                                                                                                                                                                                                                                                                                     458 GEIAAALDDIADATDQQVRTVEEV 481
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SMART; SM00283; MA; 1.
SMART; SM00091; PAS; 1.
TIGRFAMS; TIGR00229; Sensory_box; 1.
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NCBI_TaxID=64091;
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HTR15 OR VNG0958G.
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612 RADQDGDGFAVVADEVKDLADESKALAAEMQALVAEVRAQTETSVAAMDRIQERVSDGVE 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                   PLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSED
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"Signal transduction in the archaeon Halobacterium salinarium is
processed through three subfamilies of 13 soluble and membrane-bound
transducer proteins.";
Proc. Natl. Acad. Sci. U.S.A. 93:4649-4654(1996).
EMBL; U75437; AAB17882.1;
HSSP; P02942; 1QU7.
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GG; GG: 0016035; P: chemoraxis; IEA.

GG; GG: 0006935; P: chemoraxis; IEA.

GG; GG: 00016935; P: chemoraxis; IEA.

GG; GG: 00016935; P: chemoraxis; IEA.

GG; GG: 00016935; P: chemoraxis; IEA.

R InterPro; IPR004089; Chmtaxis_transd.

R InterPro; IPR004089; Mamp.

R InterPro; IPR004090; Me_chemoraxis.

R InterPro; IPR004090; Me_chemoraxis.

R InterPro; IPR004090; Me_chemoraxis.

R InterPro; IPR004090; Me_chemoraxis.

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Halobacteriaceae; Halobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                   792
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MEDLINE=96209786; PubMed=8643458;
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                                                                                                                                                                              467 IADATDQQVRTVEEV 481
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01-FEB-1997 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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                       ARIGKIHDVLGLGPDVYLGAYTRY 140
                                                                                        351 VOSLSAAAAB----IEAGNYDVDVATSRRDEIGQLFASIGSMRDALVTQAE---AAREQA
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                                                                                                                                                                                                                                                                                                                            -DSR-----HV
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SMART; SMOUO1; PAS; 1.
TIGRFAMB; TICR00229; SENSORY box; 1.
PROSITE; PSS0111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PSS0111; CHEMOTAXIS_TRANSDUC_2; 1.
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Halobacteriaceae, Halobacterium.
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GO:0004871, F:signal transducer activity;
GO:0006935; P:chemotaxis; IEA.
GO:0007165; P:signal transduction; IEA.
                                                                                                                                                                                                                                       404 TEAQQDAEADARRAEDARERAEDAKADAEALAAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : | : : | 174 LSDSTAGEAQSVSATAEEQAASMSEISDTVESLS
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InterPro; IPR004090; Me chemoCaxis.
InterPro; IPR000014; PAS domain.
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MEDLINE=97284501; PubMed=9139915;
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                                                                                                           ------VVADRGEEA--AAAVDELVARFLPML-
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"Signal transduction in the archaeon Halobacterium salinarium is
processed through three subfamilies of 13 soluble and membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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22.1%; Score 529; DB 1; Length 804;
Best Local Similarity 30.6%; Pred. No. 5.9e-15;
Matches 139; Conservative 76; Mismatches 159; Indels 8
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Halobacteriaceae; Halobacterium.
NCBI_TaxID=2242;
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Proc. Natl. Acad. Sci. U.S.A. 93:4649-4654(1996)
EMBL; U75439; AAB17884.1; -.
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GO; GO:0004871; F:signal transducer activity;
GO; GO:0005835; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004089; Chmtaxis_transd.
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VSATQEQSTAVSQLSERVDKLT 632
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                                                                                                               128 LGPDVYLGAYTRYYTGLLDALADD-
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Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
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                                                                                                       57 EYPEGILITAADGTVTHWNERFSDHMKMARSDALGEDASDVFS----TAEE-SETLPEAV 111
                                                                                                                               101 LGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEA 160
                                                                                                                                                        112 VRTGDTVEEEE------PHDVPTDSLCQYHGVPLRAPTG------DVVGSFG--V 152
                                                                                                                                                                                                        ---ORELHD-----LHETVSINVGEHLS 182
                                                                                                                                                                                                                              SLEATSODV---AERTDTWRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSED 277
                                                                                                                                                                                                                                             278 AEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNML 337
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                                    -WRLSFTGIDDDTMAALAA 52
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5 SSDMGGBATGEHLADELCEAYLGDNEDDGGBELQRLSRERDFWRHMFN------QLVA
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                Gaps
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"Signal transduction in the archaeon Halobacterium salinarium is
processed through three subfamilies of 13 soluble and membrane-bound
               98;
             Indels
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Halobacteriaceae; Halobacterium.
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Proc. Natl. Acad. Sci. U.S.A. 93:4649-4654(1996).
EMBL, US3386; AABI7519.1; -.
EMBL, US3388; T44938.
HSSP; P02942; 1QU7.
GO; GO:0016020; C::membrane; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006935; P::chemotaxis, IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004089; Me.chemotaxis.
Fram: PF00015; MCPsignal; 1.
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Last annotation update)
 Pred. No. 4.9e-15;
'; Mismatches 168;
                                     --GLDEAEIA--
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           87;
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                                    10 TADVRNGIDGHALADRI ---
30.9%;
           158; Conservative
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01-JUN-2003 (TrEMBLrel.
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 Best Local Similarity
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01-FEB-1997
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A NGW V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
NGW W.V., Kennedy S.R., Baliga N.S., Thorseon V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorseon V., Sbrogna J.,
Swartzell S., Weller K., Dahl T.A., Welli R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H.,
A lsenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Rehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
I. Genome sequence of Halobacterium species NRC-I.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
REMBLA BEOROSOS; ARG19812.1; -.
RSSP; PO2942; 1QU7.
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                                                                                                                                                                                                                                                                51; Gaps
                                                                                                                                                                                                    Length 544;
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Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCSI TaxID=64091;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                544 AA; 56922 MW; 663D8D0E43AFCA71 CRC64;
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Last annotation update)
                                                                                                                                                                                                    DB 1;
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Matches 141; Conservative 93; Mismatches 195;
                                                                                                                                                                                                21.9%; Score 523.5; DB 1
29.4%; Pred. No. 6.4e-15;
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                                                            PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
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SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
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No W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swatzell S., Weit T.D., Hall J., Danson W., Sbrogna J., Swatzell S., Weit T.D., Hough D.W., Melithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Deithauser T.A., Pack R.F., Pohlachroder M., Spudich J.W., Dale H., Bahardt T.A., Unog K.-H., Shandhardt J.C., Jung K.-H., Shandhardt J., Dennis P.P., Omer A.D., Rham M., Freitas T., Hou S., Daniels G.J., Dennis P.P., Omer A.D., Rham M., Freitas T., Hou S., Daniels G.J., Dennis P.P., Omer A.D., R. Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; R. Toco. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

R. Tenome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

R. FRISH; FR64219; FR84219.

R. GO; GO:0004871; Frsignal transduction; IEA.

GO; GO:0006835; Prsignal transduction; IEA.

GO; GO:0000535; Prsignal transduction; IEA.

GO; GO:000015; WCRSignal transduction; IEA.

InterPro: IPR004099; Chmtaxis_transd.

InterPro: IPR004099; Chmtaxis_transd.

R. Ffam; PR00672; HAMP: 1.

R. Ffam; PR00672; HAMP: 1.

R. Ffam; PR00638; PR0881900; Me_chemotaxis.

R. SMART; SM00304; HAMP; 2.

B. SMART; SM00304; HAMP; 2.

B. SMART; SM008393; Mak; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 DLTQRLDTDVDRESLAQIATAFNDMLVQLEALVDRIQATANAVDDRTHAMSASTDEIEQS 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    628 AA; 66833 MW; 98D1ECD7004ACC4B CRC64;
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PROSITE; PS50885; HAMP; 2.
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Best Local Similarity
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SEQUENCE 628 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 ---AQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALAD-DVVADRGEEAAAAVDELVA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                   21.9%; Score 523.5; DB 17; Length 643; 28.3%; Pred. No. 7.8e-15;
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                  67290 MW; 1D53F2E18BA02481 CRC64;
             GO; GO:0016020; C:membrane; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006335; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction, IEA.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004099; Me. Chemotaxis.
Pfam; PF00015; MCP8ignal; 1.
PRINTS; PR00206; MERRINSDUCR.
SMART; SM00204; HAMP; 1.
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PROSITE; PS50885; HAMP; 1.
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MEDLINE=20504483; PubMed=11016950;
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Matches 143; Conservative
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HTR16 OR VNG0614G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2242;
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                                                                                                                                                                                                 MEDLINE=2050483; PubMed=11016950;
MA WUV., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Makla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Matchell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
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BIR; E84236; E84236.
R MSSP; P02942; 10UT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.3%; Score 509.5; DB 17; Length 789; 30.6%; Pred. No. 3.9e-14; tive 80; Mismatches 165; Indels 81;
                                                   Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            789 AA; 83926 MW; ABE57215065BF4B5 CRC64;
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006935; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPRO04089; Chmtaxis_transd.
InterPro; IPRO04089; Chmtaxis_transd.
InterPro; IPRO04089; Chmtaxis_transd.
InterPro; IPRO04090; MaMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00672; HAMP; 1.

Pfam; PF00015; MCPsignal; 1.

PRINTS; PR00260; CHEMTENSDUCR.
SMART; SM00304; HAMP; 2.

SMART; SM00334; HAMP; 2.

SMART; SM00283; MA; 1.

PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.

PROSITE; PS50885; HAMP; 2.

COMDISTE POTCECOME

SEQUENCE 789 AA; 83926 MW; ABE572150658F4;
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Matches 144; Conservative
                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                 Halobacterium sp.
                           OR VNG0793G.
                                                                                                                             NCBI_TaxID=64091;
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EMBL; AF036231; AAD02052.1; -.
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                                                                                                                                      Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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GO; GO: 0016020; C: membrane; IEA.

GO; GO: 000491; F: signal transducer activity; IEA.

GO; GO: 0006935; P: c: chemotaxis; IEA.

GO; GO: 0007165; P: c: signal transduction; IEA.

InterPro; IPRO4089; Cintaxis_transd.

InterPro; IPRO4089; Cintaxis_transd.

InterPro; IPRO4090; Me_chemotaxis.

Pfam; PF0015; PR04090; Me_chemotaxis.

Pfam; PR0015; MCPsignal; 1.

PRINTS; PR00260; CHEMTRNSDUCR.

SNART; SM00304; HAMP; 2.

SNART; SM00304; HAMP; 2.

SNART; SM00304; HAMP; 2.

SNART; SNG0885; HAMP; 2.
Last sequence update)
Last annotation update)
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Search completed: August 10, 2004, 15:28:39 Job time : 60.609 secs

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OM protein - protein search, using sw model

August 10, 2004, 15:18:30; Search time 26.4879 Seconds (without alignments) 1632.058 Million cell updates/sec Run on:

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score: Title: Perfect :

Sequence:

1 VLSEGEWQLVLHVWAKVEAD......ALELFRKDIAAKYKELGYQG 153 Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* A Geneseq 29Jan04:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	Aav29391	Aaw81769	Aav69975	Aaw62270	Aaw29741	Aaw29739	Aaw29740	Aaw62271	Aaw29742	Aaw29743	Aaw62272	Aaw29744	Adc31106	Adc32817	Aaw62273	Abq04708	Abq04706	Aaq00022	Abg21418	Aaq00021	Abg21417	Aar95437	Aar95436	Abb07967	Aaw86334
SUMMARIES			391	692	975	270	741	739	740	271	742	743	272	744	901	317	273	708	907)22	118)21	117	137	136	1967	334
SU	;	ID	AAY29391	AAW81769	AAY69975	AAW62270	AAW29741	AAW29739	AAW29740	AAW6227	AAW2974	AAW29743	AAW62272	AAW29744	ADC31106	ADC32817	AAW62273	ABG04708	ABG04706	AAG00022	ABG21418	AAG00021	ABG2141	AAR95437	AAR95436	ABB07967	AAW8633
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		Match Length	153	153	153	154	154	154	154	154	154	154	154	154	166	206	154	202	231	113	334	71	107	64	09	190	201
ok	Query	Match	100.0	100.0	100.0	1.06	89.8	89.5	σ	σ	89.0	88.3	88.2	8	88.0	0.88	87.8	77.2	67.4	59.4	æ	σ'n.	31.9	30.6	30.2	27.1	27.1
	Ċ	score	794	794	794	715	713	711	711	711	707	701	700	669	669	669	697	613	532		386.5	314	S	243	240	215.5	215.5
	Result	NO.	н	7	m	4	Ŋ	9	7	Φ,	ט ְ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25

Aae04661 Haem prot Aar95435 Apomyoglo Abh07966 Himan emit			Aae04664 Haem prot Aae04669 Haem prot		Aae04673 Haem prot Aae04672 Haem prot		Aay29393 Sperm wha Aae04671 Haem prot			Abg04/0/ Novel num Abg04705 Novel hum	Human
AAE04661 AAR95435 ABB07966	ADC10192 ADC10194	AAE04662 AAE04665	AAE04664 AAE04669	AAE04670	AAE04673 AAE04672	AAE04663	AAY29393 AAE04671	AAB41929	AAE04674	ABG04705	AAW73385
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41 57 190	190	4 4 1 4 4	41 39	39	3.9 9.0 9.0	41	153	188	w n	51	141
26.8 26.8 26.8	26.8 26.8	25.7	25.4	24.9	24.4 24.1	24.1	23.9	21.6	21.4	20.7	20.5
213 213 212.5	212.5	204 203	202 198	198	194	191	189.5	171.5	170	164	163
26 27 28	29 30	31 32	33 4	35	37	38	2. 4. V O	41	2 4 4	4, 4,	45

ALIGNMENTS

AAY29391 standard; protein; 153 AA. (first entry) 01-OCT-1999 AAY29391; RESULT 1

Sperm whale myoglobin protein sequence.

Myoglobin; Mb; sperm whale; protein design; function; property; stereo structure; globular protein; detection.

Physeter sp.

JP11193297-A.

21-JUL-1999.

98JP-00283852. 06-OCT-1998; 97JP-00272431. 06-OCT-1997;

(RIKA) RIKAGAKU KENKYUSHO.

WPI; 1999-462430/39.

Method for designing artificial protein - useful for producing proteins with required functions

Japanese. Example; Page 4-5; 10pp;

The present invention describes a method for producing an ideal amino acid sequence. The method comprises: (1) preparation of one initial amino acid sequence corresponding to the structure of a protein; (2) selecting the amino acid residues optimal to each site; (3) repeating the steps of selecting the amino acid residues optimum to each sites of the total amino acid residues optimum to each sites of the total consisting of the selected amino acid sequence (N is an integer not less than 2) to give an N+1-order amino acid sequence consisting of the selected amino acid sequence comes to be same as the N+1-order amino acid sequence; and (4) selecting the resultant N-order amino acid sequence as the optimum amino acid sequence of said protein. The method can design a protein with desired functions and properties. The present sequence represents sperm whale myoglobin used in an example from the present invention where the stere structure of sperm whale myoglobin was targeted as a globular protein to detect an amino acid sequence best fit to the structure of the

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This sequence represents the MYGL protein. The invention relates to a database containing information on the amino acid (aa) sequences of proteins of which I or more biological functions are known. The database also contains additional information on the score of importance of each as residue in the whole as sequence in determining the known biological functions. The invention also relates to a method of preparing an alignment between as sequence in determining the known biological functions. The scar being is represented as the homology amongst various sites, each being identified as having a high score of importance in determining potential biological functions. The method is used to enable an efficient estimation of the biological functions (particularly sequences. Suitable proteins can then be isolated and purified by various means. This could be of considerable use in a biological and medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKPIFVKYLEFISBAIHVLHSRHP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An efficient, accurate and rapid computer database for estimating protein functions e.g. enzymatic activity, for polypeptides obtained from gene
LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHP 120
                     61 LKKHGVTVLTALGAILKKKGHHEABLKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHP 120
                                                                                                                                                                                                                                                                                                                              Protein sequence database; biological function determination; enzymatic activity; signaling activity; protein function determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEABMKASED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       context. The computerised procedure is efficient, fast and accurate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 794; DB 3; Length 153; 100.0%; Pred. No. 3e-80;
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                                                                                                     121 GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                     GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
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                                                                                                                                                                                             Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1; 26pp; Japanese.
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                                                                                                                                                                                             AAY69975 standard; protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 153; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-JP002302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-JP002302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence translation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomioka N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-136797/12.
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                                                                                                                                                                                                                                                                                                                                                                  MYGL protein.
                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9962004-A1.
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                                                                                                                                                                                                                                                                                               MYGL protein
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                                                                                                                                                                                                                               AAY69975;
       61
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                                                                                                                                                             RESULT 3
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                                                                                                                                                                                                                      61 LKKHGVTVLTALGAILKKKKGHHBAELKPLAQSHATKHKIPIKYLBFISBAIIHVLHSRHP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determination of protein biological function - comprises use of amino acid sequences database containing the relevant information.
                                                                                                                         1 VLSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein function; trypsin; bovine; homology; resemblance; whale.
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                                                         Length 153;
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Pred. No. 3e-80;
                                                                                                                                                                                                                                                                                        121 GDFGADAQGAMKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                   GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHFR; dihydrofolic acid reductase;
ribonuclease; myoglobin; database;
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Matches 153; Conservative
                                                         Query Match
Best Local Similarity 100.
Matches 153; Conservative
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Best Local Similarity
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                          Sequence 153 AA;
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Gaps

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KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISBAIIHVLHSRHPG 121

122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153

123

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AAW29741 standard; protein; 154

3 LSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPETLEKFDEFKHLKTEAEMKASEDL 62

ò οp Heart; myoglobin; Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.

Modified myoglobin protein 7.

26-OCT-1998 (first entry)

AAW29741;

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Heart; myoglobin; Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAW62270-W62273, and AAW29739-W29744, are modified synthetic horse heart myoglobin (Mb) proteins, produced by random mutagenesis of the synthetic MD gene. This present sequence contains a substitution at Lys45Glu, which has been found to enhance the peroxidase activity of the protein in general, and it may also exhibit enhanced Mn(II) peroxidase activity as well. This is due to the enhanced rate of reaction of Fe(III) Mb with hydrogen peroxide and also because the substitution at residue 45 creates a new Mn binding site which is stronger than the natural Mn binding site of Mb. These protein can be used to catalyse oxidation of a substrate by peroxidase, e.g. oxidation of Mn2+. Peroxidases are used for oxidising phenolics to polymers, as labels for e.g. antigens, antibodies or originate contains the manipulation of a configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configurati
     61 LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified myoglobin with amino acid alterations has increased peroxidase activity - used for catalysing oxidation of substrates with peroxides, e.g. in waste treatment and as label for antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith M;
                                                    GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                 Tong H,
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LEE H.
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Synthetic.
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(WANL/)
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96CA-02185605

16-SEP-1996; 16-SEP-1996;

CA2185605-A 17-MAR-1998

Synthetic.

Equus

WAN L. LEE H. BRAYER G D.

(LEEH/) BRAY/)

TONG H.

MAUK A G.

(MAUK/)

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Sequences AAM62270-W62273, and AAW29739-W29744, are modified synthetic horse heart myoglobin (Mb) proteins, produced by random mutagenesis of the synthetic Mb gene. This present sequence contains a substitution at Ile107Phe which has been shown to enhance the peroxidase activity of Mb. These protein can be used to catalyse oxidation of a substrate by peroxidase, e.g. oxidation of Mn2+. Peroxidases are used for oxidising phenolise to polymers, as labels for e.g. antigens, antibodies or oligonucleotides, in diagnostic assays and for oxidative treatment of waste streams. NB. This sequence is not given in the specification but was created from the wild type sequence given by the inventors. The position of the substitution given does not include the initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified myoglobin with amino acid alterations has increased peroxidase activity - used for catalysing oxidation of substrates with peroxides, e.g. in waste treatment and as label for antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Smith M;
                                                                                                                                                                                                                                                                                                                                                                                                                              Tong H,
                                                                                                                                                                                                                                                                                                                                                                                                                             Brayer GD,
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                                                                                                                                                                                                                                                                                                                                                                                                                             Lee H,
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Conservative

Best Local Similarity Matches 133; Conserv

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61

LSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL

90.1%; Score 715; DB 2; Length 154; 88.2%; Pred. No. 2e-71; live 8; Mismatches 10; Indels

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Query Match Best Local Similarity 88.2' Matches 134; Conservative

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Heart; myoglobin; Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
                                     KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
3 LSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPEILEKFDKFKHLKTEAEMKASEDL
                                                                                       123 DFGADAQGAMTKALELFRNDIAAKYKELGFQG 154
                                                                          122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG
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LEE H.
BRAYER G D.
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Synthetic.
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(TONG/)
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                                                                                                                                     RESULT 7
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                                                                                                                                                                                                                                                         Heart, myoglobin; Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAW62270-W62273, and AAW29739-W29744, are modified synthetic horse heart myoglobin (Mb) proteins, produced by random mutagenesis of the synthetic Mb gene. This present sequence contains a substitution at Thr39Tle which has been shown to enhance the peroxidase activity of Mb. These protein can be used to catalyse oxidation of a substrate by peroxidase, e.g. oxidation of Mat. Peroxidases are used for oxidising phenolics to polymers, as labels for e.g. antigens, antibodies or oligonucleotides, in diagnostic assays and for oxidative treatment of waste streams. MB. This sequence is not given in the specification but was created from the wild type sequence given by the inventors. The position of the substitution given does not include the initiation codon
                                            KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
       LSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPETLEKFDKFKHLKTEAEMKASEDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New modified myoglobin with amino acid alterations has increased peroxidase activity - used for catalysing oxidation of substrates with peroxides, e.g. in waste treatment and as label for antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 711; DB 2;
Pred. No. 5.5e-71;
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                                                                                                123 DFGADAQGAMTKALELFRNDIAAKYKELGFQG 154
                                                                               122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
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                                                                                                                                                                   AAW29739 standard; protein; 154
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Best Local Similarity 87.5%;
Matches 133; Conservative 5
                                                                                                                                                                                                                                      Modified myoglobin protein 5.
                                                                                                                                                                                                                                                                                                                                                                                               96CA-02185605.
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SMITH M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mauk AG,
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LEE H.
                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1996;
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                                                                                                                                                                                                                                                                                                               Equus sp.
Synthetic.
                                                                                                                                                                                           AAW29739;
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(TONG/)
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                                                                                                                                                                                                                                                                                                                         Sequences AAW62270-W62273, and AAW29739-W29744, are modified synthetic horse heart myoglobin (Mb) proteins, produced by random mutagenesis of the synthetic Mb gene. This present sequence contains a substitution at phe46Leu which has been shown to enhance the peroxidase activity of Mb. These protein can be used to catalyse oxidation of a substrate by peroxidase, e.g. oxidation of Mn2+. Peroxidases are used for oxidising phenolics to polymers, as labels for e.g. antigens, antibodies or oligonucleotides, in diagnostic assays and for oxidative treatment of waste streams. NB. This sequence is not given in the specification but
                                                                    New modified myoglobin with amino acid alterations has increased peroxidase activity - used for catalysing oxidation of substrates with peroxides, e.g. in waste treatment and as label for antigens.
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87.5%; Pred. No. 5.5e-71;
ive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                         Claim 10; Page; 23pp; English.
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Matches 133; Conservative
WPI; 1998-388655/34.
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Smith M;

Tong H,

Brayer GD,

ï Lee 2 LSEGEMQLVLHVWAKVBADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL δ

61

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10; Indels

9; Mismatches

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o O

Gaps .;

Length 154; Indels

Score 711; DB 2; L Pred. No. 5.5e-71; 9; Mismatches 10;

89.5%;

Query Match
Best Local Similarity 87.5
Matches 133; Conservative

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19 62 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153 123 DFGADAQGAMTKALELFRNDIAAKYKELGFQG 154

122

KKHGVIVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121

62

à q à g

3 LSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPETLEKFDEFKHLKTEAEMKASEDL

2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL

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Sequences AAW62270-W62273, and AAW29739-W29744, are modified synthetic horse heart myoglobin (Mb) proteins, produced by random mutagenesis of the synthetic Mb gene. This present sequence contains a substitution at Lya45Glu, which has been found to enhance the peroxidase activity of the protein in general, and it may also exhibit enhanced Mn[II] peroxidase activity as well. This is due to the enhanced rate of reaction of Fe[III] Mb with hydrogen peroxide and also because the substitution at residue 45 creates a new Mn binding site which is stronger than the natural Mn creates a new Mn binding site which is stronger than the natural Mn binding site of Mb. This protein also contains a substitution at contains a substitution at contains a substitution of creates also found to be required for Mn binding. These contoins can be used to catalyse oxidation of a substrate by peroxidase, e.g. oxidation of Mn24. Peroxidases are used for oxidising phenolics to diagnostic assays and for oxidative treatment of waste streams. NB. This sequence is not given by the inventors. The positions of the substitutions cytype sequence given by the intitiation codon
                                                   Heart; myoglobin; Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
                                KKHGVTVLTALGAILKKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
3 LSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPETLEKFDKLKHLKTEAEMKASEDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified myoglobin with amino acid alterations has increased peroxidase activity - used for catalysing oxidation of substrates with peroxides, e.g. in waste treatment and as label for antigens.
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                                                                                                  DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                     123 DFGADAQGAMTKALELFRNDIAAKYKELGFQG 154
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                                                                                                                                                                                                                 AAW62271 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                 Modified myoglobin protein 2.
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Synthetic.
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(TONG/)
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Heart, myoglobin, Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified myoglobin with amino acid alterations has increased peroxidase activity - used for catalysing oxidation of substrates with peroxides, e.g. in waste treatment and as label for antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tong H,
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                              AAW29742 standard; protein; 154 AA
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                                                                                                                          Modified myoglobin protein 8.
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                                                                                        26-OCT-1998 (first entry)
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                                                             AAW29742;
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RESULT 9
                   AAW29742
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Sequence 154 AA;

Length 154;

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(WANL/)
(LEEH/)
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                                                                                                                                                                                                           Heart, myoglobin, Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
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                                                                                                                                                                                      KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG
                                                                                                                           2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
                                                 Gaps
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Score 707, DB 2; Length 154; Pred. No. 1.5e-70; 9; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                            DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                      123 DFGADAOGAMTKALELFRNDIAAKYKELGFOG 154
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       89.0%;
86.8%;
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                                                 Matches 132; Conservative
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                                Similarity
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LEE H.
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         Query Match
Best Local &
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Sequence 154 AA;

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                                                                                                                                                Heart; myoglobin; Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
                                                                                                                               62 KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
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                                                                                   LSEGEWOLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
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                                12; Indels
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Score 701; DB 2;
Pred. No. 7.2e-70;
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                                                                                                                                                                                                DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                             123 DFGADAQGAMTKALELFRNDIAAKYKELGFQG 154
                                  9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96CA-02185605.
88.3%;
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                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ή,
 Query Match
Best Local Similarity 86.2
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-388655/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRAYER G D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mauk AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAUK A G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WAN L.
LEE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMITH M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TONG H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                 26-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA2185605-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equus sp.
Synthetic.
                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                 AAW62272;
                                                                                                    m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRAY/)
(TONG/)
(SMIT/)
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Mb with hydrogen peroxide and also because the substitution at residue 45 creates a new Mn binding site which is stronger than the natural Mn binding site of Mb. This sequence also contains substitutions at Thr391le, Phe46Leu, and Ile107Phe, which have been shown to enhance the peroxidase activity of Mb.These protein can be used to catalyse oxidation of a substrate by peroxidase, e.g. oxidation of Mn2+. Peroxidases are used for oxidising phenolics to polymers, as labels for e.g. antigens, antibodies or oligomuclectides, in diagnostic assays and for oxidative treatment of waste streams. NB. This sequence is not given in the specification but was created from the wild type sequence given by the inventors. The positions of the substitutions given do not include the

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Gaps

0;

13;

8; Mismatches

Length 154; Indels

Score 699; DB 2; Pred. No. 1.2e-69;

88.0%; 86.2%;

Query Match
Best Local Similarity 86.2
Matches 131; Conservative

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initiation codon Sequence 154 AA;

61 62

LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL 3 LSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPEILEKFDELKHLKTEAEMKASEDL 62 KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121

122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153

^

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polymers, as labels for e.g. antigens, antibodies or oligonucleotides, in diagnostic assays and for oxidative treatment of waste streams. NB. This sequence is not given in the specification but was created from the wild type sequence given by the inventors. The positions of the substitutions given do not include the initiation codon
                                                                                                                                                                     62 KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEPISEAIIHVLHSRHPG 121
                                                                                                                                                                                    Heart; myoglobin; Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
                                                                                                                                 19
                                                                                                                                                     62
                                                                                                                                           2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
                                                                                                             Gaps
                                                                                                             ..
                                                                                     Score 700; DB 2; Length 154;
Pred. No. 9.3e-70;
                                                                                                          11; Indels
                                                                                                                                                                                                                 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                     123 DFGADAQGAMTKALELFRNDIAAKYKELGFQG 154
                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                             Ā
                                                                                                                                                                                                                                                                                       AAW29744 standard, protein, 154
                                                                                                                                                                                                                                                                                                                                                       Modified myoglobin protein 10.
                                                                                   88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96CA-021B5605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96CA-02185605
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                              Best Local Similarity 86.8
Matches 132; Conservative
                                                                 Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1996;
                                                                                                                                                                                                                                                                                                                                   26-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA2185605-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Equus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                             AAW29744;
                                                                                     Query Match
                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                              AAW29744
  88866666
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New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                           neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 22q13.1.
                                                                                                                                                                                     Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J,
Wang Z,
                                                                                                                                                              Human novel polypeptide sequence, SEQ ID NO:1188.
Xue AJ, Zhao QA,
Ma Y, Asundi V,
                                                                          ADC31106 standard; protein; 166 AA.

    Ren F, Xue
    Wang D, Ma
    Drmanac RT;

                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-2001; 2001US-0324631P
                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-371981/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haley-Vicente D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADC30135
                                                                                                                                                                                                                                                                                                                                           WO2003029271-A2.
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                         10-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang TY,
Zhou P, G
                                                                                                     ADC31106;
                                                RESULT
```

Sequences AAW62270-W62273, and AAW29739-W29744, are modified synthetic horse heart myoglobin (Mb) proteins, produced by random mutagenesis of the synthetic Mb gene. This present sequence contains a substitution at Lys45Glu, which has been found to enhance the peroxidase activity of the protein in general, and it may also exhibit enhanced Mn(II) peroxidase activity as well. This is due to the enhanced rate of reaction of Fe(III)

substrates with

New modified myoglobin with amino acid alterations has increased

Smith M;

Tong H,

Brayer GD,

Ħ, Lee

Mauk AG, SMITH M. TONG H.

Wan L,

BRAYER G D.

(LEEH/) (BRAY/) (TONG/)

(SMIT/)

MAUK A G.

(MAUK/)

(WANL/)

WPI; 1998-388655/34.

peroxidase activity - used for catalysing oxidation of substr peroxides, e.g. in waste treatment and as label for antigens.

Claim 21; Page; 23pp; English.

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DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                  13; Mismatches
          Claim 20; SEQ ID NO 1188; 1185pp; English
                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                           ADC32817 standard; protein; 206 AA
                                                                                                                                                                                                                                                                                                                               18-DEC-2003 (first entry)
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                            Local Similarity
ses 129; Conserv
                                                                                                                                                                                              Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                     ADC32817;
                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                 135
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                 RESULT 14
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N-PSDB; ADC32050 Into invention also relates to 9.1 movet number cure sequences (ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the nuvention also relates to nucleic acid sequences over 99% identical with cover the noveh human cDMAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of invention detecting a compound which binds to a polypeptide of the invention. The invention further discloses methods to a polypeptide of the invention. The invention a method for the identification of compounds that modulate the and/or monoclonal antibodies for carrying out the methods of the invention methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide, and 767 contig sequences corresponding to the cDNA sequences of the invention are abcribed and the polynucleotide and/or polypeptide, and 767 contig sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the contification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease. Alzaheimer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at The invention relates to 971 novel human cDNA sequences (ADC29919-

KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121 61 15 LSDGEWQLVLNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDKFKHLKSEDEMKASEDL 74 2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL Gaps 0; 88.0%; Score 699; DB 7; Length 166; 84.9%; Pred. No. 1.3e-69; 10; Indels

Human; diagnostic; drug screening; forensics; gene mapping; bodiversity assessment. Parkinson; disease; Alzheimer's disease; neurodegenerative diseases; namema, platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; cancer; neurodest marker; food supplement, antiparkinsonian; nootropic; neuroporotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antinflammatory; cytostatic; Human novel contig-encoded polypeptide sequence, SEQ ID NO:2899.

Wehrman T; Wang J, Wang Z, W Wang ? Xue AJ, Zhao QA, Ma Y, Asundi V, gene therapy; chromosome 22q13.1. J, Ren F, Xue , Wang D, Ma Drmanac RT; 24-SEP-2002; 2002WO-US030474. 24-SEP-2001; 2001US-0324631P WPI; 2003-371981/35. Zhang J, Ghosh M, (HYSE-) HYSEQ INC. Haley-Vicente D, WO2003029271-A2. Homo sapiens. 10-APR-2003. Tang TY,

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer.

Example 2; SEQ ID NO 2899; 1185pp; English.

The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The invention allow relates to nucleic acid sequences over 99% identical with the newel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of adainst a polypeptide of the invention; and methods of polynucleotides or polypeptides of the invention; and methods of invention in multibodies of carriving out the methods of the invention. The invention further discloses methods of peventing, treating or and/or monofolonal antibodies for carrying out the methods of the invention invention; methods for the identification of compounds that modulate the expression or activity of the polymucleotide and/or polypeptide; and 767 contigs sequences corresponding to the cDNA sequences of the invention (ADC31661-ADC32627) and the polypeptides encoded by the contigs (ADC32628 ADC333394). The mucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the classification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of disease and other neurodegenerative diseases, anaemia, platelet cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptide are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence encoded bolypeptide sequence used in an example of the invention. Note: or moded polypeptide sequence used in an example of the invention. The present sequence of the invention. The present sequence of the plant did not form part of the promiser. specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Gaps 88.0%; Score 699; DB 7; Length 206; 84.9%; Pred. No. 1.8e-69; Indels 10; 13; Mismatches Best Local Similarity 84.9 Matches 129, Conservative Query Match

Sequence 206 AA;

55 LSDGEWQLVLNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDKFKHLKSEDEMKASEDL 114 2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL

ð g ò

62 KKHGVIVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121

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115 KKHGATVLTALGGILKKKCHHEAEIKPLAQSHATKHKIPVKYLEFISECIIQVLQSKHPG 174
                                                                                                                                                                                 Brayer GD,
                                        AAW62273 standard; protein; 154 AA.
                                                                                                                                                                                                                    Claim 23; Page; 23pp; English.
                                                                    Modified myoglobin protein 4.
                                                                                                                               96CA-02185605
                                                                                                                                        96CA-02185605
                                                           (first entry)
                                                                                                                                                                                 Ή
                                                                                                                                                                                 ree
                                                                                                                                                                                          WPI; 1998-388655/34.
                                                                                                                                                          LEE H.
BRAYER G D.
                                                                                                                                                 MAUK A G.
                                                                                                                                                                                Mauk AG,
                                                                                                                                                                       SMITH M.
                                                                                                                                                                                                                                                                                                                     Sequence 154 AA;
                                                                                                                                                     WAN L.
                                                                                                                                                                   TONG H.
                                                           26-OCT-1998
                                                                                                                              16-SEP-1996;
                                                                                                                                        16-SEP-1996;
                                                                                                            CA2185605-A
                                                                                                                      17-MAR-1998,
                                                                                               Equus sp.
Synthetic.
         122
                                                  AAW62273;
                                                                                                                                                                   (TONG/)
                                                                                                                                                 MAUK/)
                                                                                                                                                          (LEEH/)
(BRAY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heart; myoglobin; Mb; random mutagenesis; peroxidase activity; Fe(III); Mn(II) peroxidase activity; hydrogen peroxide; Mn binding site; catalyse; phenolic; polymer; antigen; antibody; diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New modified myoglobin with amino acid alterations has increased peroxidase activity - used for catalysing oxidation of substrates with peroxides, e.g. in waste treatment and as label for antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith M;
DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                          175 DFGADAQGAMNKALELFRKDMASNYKELGFQG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tong H,
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Gaps

· 0

87.8%; Score 697; DB 2; Length 154; 86.2%; Pred. No. 2e-69; iive 10; Mismatches 11; Indels

Query Match
Best Local Similarity 86.2°
Matches 131, Conservative

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KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
                                        62
      61
  LSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
                        122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                           123 DFGADAQGAMTKALELFRNDIAAKYKELGFQG 154
                                                                                                                                                                                                                                                         Search completed: August 10, 2004, 15:26:14
                                                                                                                                                                                                                                                                           Job time : 27.4879 secs
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                Copyright
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using sw model OM protein - protein search,

August 10, 2004, 15:23:41 Run on:

, Search time 7.77966 Seconds
(without alignments)
1015.311 Million cell updates/sec

US-09-455-978B-76

794 1 VLSEGEWQLVLHVWAKVEAD......ALELFRKDIAAKYKELGYQG 153 Title: Perfect score:

BLOSUM62 Scoring table: Sequence:

389414 segs, 51625971 residues Searched:

Gapop 10.0 , Gapext 0.5

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

/cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:* Issued Patents AA:* 1 2 E 4 E 9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	794	100.0	153		US-08-992-176-7	Sequence 7. Appli
7	778.5	98.0	152	٣	US-08-992-176-10	10
٣	717	90.3	154	~	-08-71	11
4	969	87.7	154	٣	US-08-817-787-18	18
ഗ	584	73.6	113	N	US-08-710-330A-2	
9	525	66.1	113	~	US-08-710-330A-1	H
7	515	64.9	113	7	US-08-710-330A-5	'n
α ο	505	63.6	113	N	US-08-710-330A-4	Sequence 4, Appli
σ	504	63.5	113	7	US-08-710-330A-3	'n
10	240	30.2	9	ᡤ	US-08-817-787-22	22.
11	240	30.2	64	٣	US-08-817-787-24	24.
12	213	26.8	57	m	-08-817-787	20,
13	162	20.4	141	Н	US-08-240-712-18	18,
14	162	20.4	141	Н	US-08-443-890-18	18,
15	162	20.4	141	7	US-08-484-686B-65	65,
16	162	20.4	141	ო	US-08-463-160B-66	9
17	162	20.4	141	2	PCT-US92-09752-18	18,
18	152	19.1	141	ო	US-09-058-562-18	-
19	150	18.9	146	4	US-09-353-719-1	1, 7
20	140	17.6	141	7	-08-627-	Sequence 21, Appl
21	140	17.6	141	N	US-08-535-882A-21	21,
22	140	17.6	141	m	US-08-316-424A-7	7, 1
23	140	17.6	141	m	US-09-005-546-21	21,
24	140	17.6	141	4	US-08-477-669-7	7, 1
25	140	17.6	141	4	US-10-128-581-26	26,
56	135	17.0	146	7	US-08-619-708A-4	4, 1
27	128	16.1	141	7	US-08-627-173-19	Sequence 19, Appl

Sequence 19, Appl	Sequence 5, Appli	Sequence 19, Appl	Sequence 5, Appli	Sequence 24, Appl	Sequence 22, Appl		8, A	22,	8	27,	Sequence 24, Appl	24,	22,	24,	7	21,	21,
US-08-535-882A-19	US-08-316-424A-5	US-09-005-546-19	US-08-477-669-5	US-10-128-581-24	US-08-627-173-22	US-08-535-882A-22	US-08-316-424A-8	US-09-005-546-22	US-08-477-669-8	US-10-128-581-27	US-08-240-712-24	US-08-443-890-24	US-09-058-562-22	PCT-US92-09752-24	US-08-619-708A-2	US-08-240-712-21	US-08-443-890-21
0	m	m	4	4	7	N	m	~	4	4	-	-	m	S	7	Н	н
141	141	141	141	141	146	146	146	146	146	146	146	146	146	146	141	146	146
16.1	16.1	16.1	16.1	16.1	16.0	16.0	16.0	16.0	16.0	16.0	15.7	15.7	15.7	15.7	15.6	15.6	15.6
128	128	128	128	128	127	127	127	127	127	127	125	125	125	125	124	124	124
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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61 LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIHVLHSRHP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
                                                              GENERAL INFORMATION:
APPLICANT: TOH, Hiroyuki
TITLE OF INVENTION: STRUCTURAL ALIGNMENT METHOD MAKING USE OF A DOUBLE
TITLE OF INVENTION: STRUCTURAL ALIGNMENT METHOD MAKING USE OF A DOUBLE
TITLE OF INVENTION: DYNAMIC PROGRAMMING ALGORITHM
FILE REFERENCE: 9200-0001-2
CURRENT APPLICATION NUMBER: US/08/992,176
CURRENT FILING DATE: 1997-12-17
BARLIER APPLICATION NUMBER: 198-340727
BARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description of Artificial Sequence:alpha-protein (1mbc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 794; DB 3;
Pred. No. 2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                        Sequence 7, Application US/08992176
Patent No. 6125331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
US-08-992-176-7
US-08-992-176-7
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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RESULT 2
US-08-992-176-10
S-08-992-176-10
S-08-992-176-10
Sequence 10, Application US/08992176
Patent No. 6125331
GENERAL INFORMATION:
APPLICANT: TOH, Hiroyuki
TITLE OF INVENTION: STRUCTURAL ALIGNMENT METHOD MAKING USE OF A DOUBLE
TITLE OF INVENTION: DYNAMIC PROGRAMMING ALGORITHM
FILE REFERENCE: 9200-0001-2 GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153 121 q

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; TOPOLOGY: linear
US-08-710-330A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHS-HP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VĽSEGEWOLVĽHVWAKVEADVAGHGÓDÍLIRLFKSHPETLEKFDRFKHLKTEAEMKÁSED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence:alpha-protein; OTHER INFORMATION: (1mbc)
US-08-992-176-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08710330A

Patent No. 5854041

GENERAL INFORMATION:

APPLICANT: Lee, Hung

APPLICANT: Smith, Michael

APPLICANT: Smith, Michael

APPLICANT: Tong, Harry

APPLICANT: Wan, Lianglu

ITITLE OF INVENTION: MYOGLOBIN WITH PEROXIDASE ACTIVITY

WUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MELLUN: ...
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPELICATION NUMBER: US/08/710,330A
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMM: GAY, David A. 39,200
REFERENCE/DOCKET NUMBER: P-SM 2262
TELEPOMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATI
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Pred. No. 1.1e-79;
0; Mismatches 0;
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDFGADAQGAMKALELFRKDIAAKYKELGYQG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
CURRENT APPLICATION NUMBER: US/08/992,176
CURRENT FILING DATE: 1997-12-17
EARLIER APPLICATION NUMBER: JP 8-340727
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 10
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.0%;
Best Local Similarity 99.3%;
Matches 152; Conservative (
                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 154 amino acida
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-710-330A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pack, Peter
APPLICANT: Lupas, Andrei
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
TITLE OF INVENTION: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                     2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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84.2%; Pred. No. 2e-70;
tive 14; Mismatches 10; Indels
  DB 2; Length 154;
                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
COMPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,787
FILING DATE: 23-SEP-1997
CLASSIFICATION NUMBER: PCT/EP95/04117
FILING DATE: PRICATION NUMBER: PCT/EP95/04117
FILING DATE: 20-OCT-1994
ATTOKNEY/AGRATION NUMBER: EP 94 11 6558.1
FILING DATE: 20-OCT-1994
ATTOKNEY/AGRATION NUMBER: SP 77,794
REGISTRATION NUMBER: Z,7,794
REGISTRATION NUMBER: Z,7,794
REGISTRATION NUMBER: Z,7,794
REGISTRATION NUMBER: Z,7,794
REFERENCE/DOCKET NUMBER: Z,7,794
REFERENCE/DOCKET NUMBER: Z,7,794
REFERENCE/DOCKET NUMBER: Z,7,794
Score 717; DB 2;
Pred. No. 9e-73;
9; Mismatches
                                                                                                                                                                                                                                                                                                             122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                                           123 DFGADAQGAMTKALELFRNDIAAKYKELGFQG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: FISH & NEAVE STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-817-787-18; Sequence 18, Application US/08817787; Patent No. 6294353; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTER.STICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
Query Match 90.3%;
Best Local Similarity 88.2%;
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 84.2%
Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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Sequence 1, Application US/08710330A
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                                        3 LSDGEWQLVLNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDKFWHLKSEDEMKASEDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLSEGEWOLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED 60
             2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brayer, Gary D.
APPLICANT: Lee, Hung
APPLICANT: Mauk, Grant A.
APPLICANT: Mauk, Grant A.
APPLICANT: Smith, Michael
APPLICANT: Tong, Harry
APPLICANT: Wan, Lianglu
TITLE OF INVENTION: MYOGLOBIN WITH PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,330A
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     red. No. 5e-58;
Mismatches 0;
                                                                                                                                                                                  122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                             123 DFGADAEGAMNKALELFRKDMASNYKELGFQG 154
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                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08710330A Patent No. 5854041 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT IRFORMATION:
NAME: GAY, DAVIG A.
REGISTRATION NUMBER: 39,200
REFRENCE/DOCKET NUMBER: P-SM
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9901
TELEFAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08; Pre
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STREET: 43/CCITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-710-330A-2
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Best Local Similarity
Matches 113; Conserv
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RESULT 6 US-08-710-330A-1

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2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.1%; Score 525; DB 2; Length 113; Best Local Similarity 87.5%; Pred. No. 2.1e-51; Matches 98; Conservative 7; Mismatches 7; Indels
Sequent No. 5854041

GENERAL INFORMATION:
APPLICANT: Brayer, Gary D.
APPLICANT: Lee, Hung
APPLICANT: Smith, Michael
APPLICANT: Smith, Michael
APPLICANT: Wan, Lianglu
TITLE OF INVENTION: MYOGLOBIN WITH PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brayer, Gary D.
APPLICANT: Lee, Hung
APPLICANT: Mauk, Grant A.
APPLICANT: Smith, Michael
APPLICANT: Tong, Harry
APPLICANT: Tong, Harry
APPLICANT: Wan, Lianglu
TITLE OF INVENTION: MYOGLOBIN WITH PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/710,330A FILING DATE: 16-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                    E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-710-330A-5; Sequence 5, Application US/08710330A; Patent No. 5854041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: GAY, David A.
REGISTRATION NUMBER: 39,200
REFRENCE/DOCKET NUMBER: P-SM
TELECOMMUNICATION INFORMATION:
TELEFONE: (619) 535-9001
TELEFONE: (619) 535-9001
TELEFONE: (619) 535-901
TELEFONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSE: Campbell
                                                                                                                                                                                                                                                                                                        STREET: 4370 La JC
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Diego
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                           92122
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                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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2 LSDGEWQLVLNAWGKVEADVAGHGQEVLIRIFIGHPETLEKFDKFKHLKTEAEMKASEDL 61
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                                                                                                                                                                                                                                                                                                                     2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIH 113
                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                        Query Match 63.6%; Score 505; DB 2; Length 113; Best Local Similarity 83.0%; Pred. No. 3.7e-49; Matches 93; Conservative 11; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lee, Hung
APPLICANT: Mauk, Grant A.
APPLICANT: Smith, Michael
APPLICANT: Tung, Harry
APPLICANT: Wan, Lianglu
TITLE OF INVENTION: MYOGLOBIN WITH PEROXIDASE ACTIVITY
NUMBER OF SOUGHNES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATEMIN PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,330A
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GAY, DAVIG A.
REGISTRATION NUMBER: 39,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 504; DB 2; L
83.9%; Pred. No. 4.8e-49;
Live 9; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/08710330A; Patent No. 5854041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
(619) 535-9001
                                                                                   LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brayer, Gary D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.99
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Diego
STATE: California
                                                                                                                                                             ; TOPOLOGY: linear
US-08-710-330A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-710-330A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-710-330A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LSDGEWOLVLNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDKFKHLKSEDEMKASEDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Brayer, Gary D.
APPLICANT: Lee, Hung
APPLICANT: Mauk, Grant A.
APPLICANT: Smith, Michael
APPLICANT: Smith, Michael
APPLICANT: Wan, Lianglu
TITLE OF INVENTION: WYOGLOBIN WITH PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell : -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,330A
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: GAY, DAVIG A.
REGISTRATION NUMBER: 39,200
REFERENCE/DOCKET NUMBER: 39,200
REFERENCE/COKET NUMBER: 35,200
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION POR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDENESS:
TOOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,330A
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 515; DB 2;
Pred. No. 2.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 39,200
REFERENCE/DOCKET NUMBER: P-SM 2262
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08710330A
Patent No. 5854041
GENERAL INFORMATION:
APPLICANT: Brayer, Gary D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.9%;
85.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.6
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIF: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                       ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAY, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-710-330A-5
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    COUNTRY:
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PRIOR APPLICATION DATA:
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2 LSDGEWQAVLNAWGKVEADVAGHGQEVLIRLFTGHPETLEKFDKFKHLKTEAEMKASEDL 61
                                                                                                                                                                                          Sequence 22, Application US/08817787
Patent No. 6294353
CENERAL INFORMATION:
APPLICANT: Pack, Peter
APPLICANT: Lupas, Andrei
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
TITLE OF INVENTION: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08817787
Patent No. 629453
GENERAL INFORMATION:
APPLICANT: Pack, Peter
APPLICANT: Lupas, Andrei
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
TITLE OF INVENTION: TECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                       62 KKHGNIVLTALGGILKKKGHHEAEVKHLAESHANKHKVPIKYLEFISDAIIH 113
                                           KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIH 113
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Pred. No. 8.6e-20;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/817,787 FILING DATE: 23-SEP-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-5EP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04117
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 6558.1
FILING DATE: 20-0CT-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.2%;
Best Local Similarity 90.2%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-596-900
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-817-787-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-08-817-787-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-817-787-24
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GENERAL INFORMATION:
APPLICANT: Pack, Peter
APPLICANT: Daps, Andrei
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
TITLE OF INVENTION: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1.21 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 IPIKYLEFISEALIHVLHSRHPGDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 IPVKXVEFISECIIQVLQSKHPGDFGADAEGAMNKALELFRKDMASNYKELGFQG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.2%; Score 240; DB 3; Length 64; 80.0%; Pred. No. 9.4e-20; Live 7; Mismatches 4; Indels
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/817,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/817,787
FILING DATE: 23-SEP-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                 FILING DATE: 23-SEP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04117
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 6558.1
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 21-2-96-9000
                 ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                              UMBER: US/08/817,787
23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08817787 Patent No. 6294353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                    10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-817-787-20
                                                                                                              COUNTRY:
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62 KKHGVIVLTALGAILKKKKGHHEABLKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
                                                                                                                                                                                                                                                                                                                                                                                                       2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL 61
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                         Gaps
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                                                                                          Length 141;
                                                                                                                                                         70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCOMMATION:
GENERAL INCOMMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: ANTERNS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION NUMBER: US 08/240,712
FILING DATE: US-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,0055
REGISTRATION NUMBER: 28,0055
                                                                                          Score 162; DB 1;
Pred. No. 1.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                             29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 DFGADAQGAMNKALELFRKDIAAKYK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: ANDERSON=6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFRAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-08-443-890-18
Sequence 18, Application US/08443890
Patent No. 5739011
                                                                                          Query Match
Best Local Similarity 28.1%;
Matches 41; Conservative 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 amino acids
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Best Local Similarity 28.11
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-08-443-890-18
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
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US-08-240-712-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/08240712;
Patent No. 5599907
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
CITY: Washington
CITY: Washington
CITY: Washington
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILING DATE: 09-MAY-1994
CLASSIFICATION NUMBER: PCT/US92/09752
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: ANDERSON-6
REGISTRATION NUMBER: ANDERSON-6
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REGISTRATION NUMBER: ANDERSON-6
REGISTRATION NUMBER: ANDERSON-6
APPLICALL...
PRIGE DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 6558.1
FILING DATE: 20-0CT-1994
ATTORNEY, AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
FERFERENCE/DOCKET NUMBER: MORPHO/1
TELECOMMUNICATION INFORMATION:
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEFAX: 248633
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-550
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-817-787-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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COUNTRY:
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US-08-240-712-18
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62 KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
                                                                                                                                     58 --HGSKVVAAVGDAVKSIDDIGGALSKLSELHAYILRVDPVNFKLISHCLLVTLAARFPA 115
                                |::| ::::|||;
|LKTERTIIVSMWAKISTQADTIGTETLERLFLSHPQTKTYFPHFDLHPGSAQLRA---- 57
LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL 61
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                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/08484686B
Patent No. 5827693
GENERAL INFORMATION:
APPLICANT: De Angelo, Joseph
APPLICANT: Bajwa, Wajeeh
TITLE OF INVENTION: Expression of Recombinant Hemoglobin and
TITLE OF INVENTION: Hemoglobin Variants in Yeast
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2711
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,686B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.4%; Score 162; DB 2; L 28.1%; Pred. No. 1.6e-10; active 29; Mismatches 70;
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                                                                                                                                                                                                                                       116 DFTAEAHAAWDKFLSVVSSVLTEKYR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/484,686B FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: 425 PRIOR APPLICATION DATA: 425 PRIOR APPLICATION NUMBER: US 08/368,407 FILING DATE: 29-DEC-1994 PRIOR APPLICATION DATA: 4007/876,290 PRIOR APPLICATION NUMBER: US 07/876,290 PRIOR APPLICATION DATA: 4007/684,611 PRIOR APPLICATION DATA: 41070RNER: US 07/684,611 PATTORNER; US 07/684,611 ATTORNER; ESINTOÉE, GERALD US.
                                                                                                                                                                                            122 DFGADAQGAMNKALELFRKDIAAKYK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20,823
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TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-909
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERICTICS: LENGTH: 141 amino acids STRANDEDNESS:
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Flintoft, Gerald J. REGISTRATION NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-484-686B-65
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Search completed: August 10, 2004, 15:30:20 Job time : 8.77966 secs

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; Search time 22.2276 Seconds (without alignments) 2159.184 Million cell updates/sec
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1 VLSEGEWQLVLHVWAKVEAD......ALELFRKDIAAKYKELGYQG 153
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/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
/ cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1291235 seqs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listing first 45 summaries
                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                             August 10, 2004, 15:28:46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                            US-09-455-978B-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 106, App	Sequence 19, Appl Sequence 17. Appl	Sequence 7. Appli	Sequence 26, Appl	Sequence 28, Appl	Sequence 4, Appli	Sequence 102, App	Sequence 227247,	Sequence 189, App	Sequence 5, Appli	Sequence 24, Appl	Sequence 26. Appl	Sequence 8, Appli	Sequence 27, Appl
SUMMARIES	US-10-408-765A-106	US-10-289-009-17	US-09-839-164-7	US-10-128-581-26	US-10-463-699-28	US-10-289-009-4	US-10-378-029-102	US-10-424-599-227247	US-10-205-219-189	US-09-839-164-5	US-10-128-581-24	US-10-463-699-26	US-09-839-164-8	US-10-128-581-27
DB	16	15	6	14	16	15	15	12	14	6	14	16	6	14
% Query Match Length DB	154	31	141	141	141	31	154	142	142	141	141	141	146	146
% Query Match	87.7	19.1	17.6	17.6	17.6	16.8	16.8	16.6	16.6	16.1	16.1	16.1	16.0	16.0
Score	696	152	140	140	140	133	133	132	132	128	128	128	127	127
Result No.	40	m	4	Ŋ	9	7	80	თ	10	11	12	13	14	15

Sequence 29, Appl Sequence 20, Appl Sequence 17, Appl Sequence 6, Appli Sequence 25, Appli	Sequence 27, Appl Sequence 8, Appli Sequence 2, Appli Sequence 14, Appl Sequence 18, Appl	Sequence 8, Appli Sequence 31, Appl Sequence 21, Appl Sequence 8, Appli Sequence 3, Appli Sequence 7, Appli	4 4	Sequence 25, Appl Sequence 319, Ap Sequence 12, Appl Sequence 21, Appl Sequence 21, Appl Sequence 16, Appl Sequence 84, Appl Sequence 13, Appl
-463-699-2 977-577-20 977-577-17 839-164-6 -128-581-2	9		D D	6 US-10-463-699-25 6 US-10-408-765A-3019 8 US-10-289-009-12 1US-09-977-577-21 US-09-977-577-16 6 US-10-408-765A-84 5 US-10-289-009-13
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16.0 15.7 15.6 15.1	151 141 1441 1441 1441	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	13.00.00	13.0 12.7 12.7 12.6 12.6 12.5 12.3
127 125 124 120 120	120 114 112 112	112 112 112 112	111 104 103 103 103	100 1001 1001 998
16 17 18 19 20	22 22 24 24 55	26 27 29 30 31	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	8 6 6 4 4 4 4 4 4 5 5 6 6 6 6 6 6 6 6 6 6

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                  GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Farly, Eoin D.
APPLICANT: Farly, Eoin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: 10 DANTIFIED IN THE MITOCHONDRIAL PROTEOME
CURRENT FILLING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077-04-04
SEQ ID NO 106
SEQ ID NO 106
LENGTH: 154
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84.2%; Pred. No. 2.3e-69;
ive 14; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                  Sequence 106, Application US/10408765A
Publication No. US20040101874A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo
US-10-408-765A-106
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Best Local S:
Matches 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRF--KHLKTEAEMKAS
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09839164
Patent No. US20020098583A1
GENERAL INFORMATION:
APPLICANT: KOZLOV, VLADIMIR
TSYRLOVA, VIRBNA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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                                                                         Length 31;
                                                                                                                        Indels
OTHER INFORMATION: myoglobin tryptic polypeptide #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
                                                                         Score 152; DB 15;
Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/477,668
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/316,424
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: PCT/US94/03349
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 08/040,942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,164
FILING DATE: 23-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                            103 YLEFISEAIIHVLHSRHPGDFGADAQGAMNK 133
                                                                                                                                                                                                         1 YLEFISDAIIHVLHSKHPGDFGADAQGAMTK 31
                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-MAR-1993
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                      Query Match
Best Local Similarity 90.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Conservative
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Best Local Similarity
          ; UTHER INFORM
US-10-289-009-17
                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-839-164-7
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TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES
FILE REFERENCE: MOSSTRUP-IN.

GURRENT APPLICATION NUMBER: US/09/977,577

CURRENT FILING DATE: 2001-10-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Labeling Reagent and Methods of Use FILE REPERENCE: 021288-000230US
CURRENT APPLICATION NUMBER: US/10/289,009
CURRENT PLING DATE: 2003-04-01
PRIOR PLING DATE: 2001-11-05
PRIOR PLING DATE: 2001-11-05
PRIOR PLING DATE: 2001-11-05
PRIOR PLING DATE: 2002-06-03
PRIOR FILING DATE: 2002-06-03
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 29
SEQ ID NOS: 29
SEQ ID NO 17
LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 20.4%; Score 162; DB 9;
1 Similarity 28.1%; Pred. No. 7.4e-10;
41; Conservative 29; Mismatches 70
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: US 60/270,120
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: DK PA 2001 00039
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: DK PA 2000 01543
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 DFGADAQGAMNKALELFRKDIAAKYK 147
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116 DFTAEAHAAWDKFLSVVSSVLTEKYR 141
                                                                                                                                             Sequence 19, Application US/09977577
Patent No. US20020155995A1
GENERAL INFORMATION:
APPLICANT: MOESTRUP, Soren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/10289009
Publication No. US20030228700A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Peters, Eric C.
APPLICANT: Brock, Ansgar
APPLICANT: Ericson, Christer
APPLICANT: IRM LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-09-977-577-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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US-10-289-009-17
                                                                                                                        -09-977-577-19
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LENGTH: 141
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WOLPE, STEPHEN D.
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                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                            STATE: VIRGINIA COUNTRY: U.S.A.
                                                    NUMBER OF SEQUENCES:
                                                                                                                              CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-463-699-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                    TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL. FOR INHIBITING STEM CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VLSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRF--KHLKTEAEMKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 140; DB 14;
27.6%; Pred. No. 2.1e-07;
tive 20; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION INTO CUINTIONNINA
PRIOR APPLICATION NUMBER: US 09/617,840
FILING DATE: 17-JUL-2000
APPLICATION NUMBER: US 09/005,546
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
APPLICATION NUMBER: US 08/316,424
FILING DATE: 30-SEP-1995
APPLICATION NUMBER: PCT/US94/03349
FILING DATE: 29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 HSRHPGDFGADAQGAMNKALELFRKDIAAKYK 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/040,942
FILING DATE: 31-MAR-1993
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,581
FILING DATE: 24-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSER: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                          Application US/10128581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/10463699; Publication No. US20040081640A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 141 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                   APPLICANT: TSYRLOVA, IRENA WOLPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Conservative
                                                                                                                                                                             SEQUENCES:
                                                                                                                                                                                                                                                                       STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 42; Conserva
                       US-10-128-581-26
; Sequence 26, Applicatio; Publication No. US20031; GENERAL INFORMATION:
                                                                                                                                                                             NUMBER OF
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         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 EDLKKHGVTVLTALGAILKKKKGHHE---AELKPLAQSHATKHKIPIKYLEFISEAIIHVL 115
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TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL FOR INHIBITING STEM CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VLSEGEWQLVLHVWAKVEADVAGHCQDILIRLFKSHPETLEKFDRF--KHLKTEAEMKAS
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APPLICANT: Brock, Ansgar
APPLICANT: Ericson, Christer
APPLICANT: IRM LLC
ITTLE OF INVENTION: Labeling Reagent and Methods of Use
FILE REFERENCE: 021288-000230US
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/10/463,699
FILING DATE: 10-Unr-2003
CLASSIFICATION NUMBER: US/10/128,581
FILING DATE: 24-APR-2002
APPLICATION NUMBER: US 09/617,840
FILING DATE: 24-APR-2002
APPLICATION NUMBER: US 09/617,840
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: US 08/535,882
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: US 08/535,882
FILING DATE: 38-SEP-1995
APPLICATION NUMBER: US 08/316,424
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: US 08/316,424
FILING DATE: 29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 HSRHPGDFGADAQGAMNKALELFRKDIAAKYK 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/040,942
FILING DATE: 31-MAR-1993
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                       ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                             ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: 1,44 MB Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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SEQ ID NO 227247
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APPLICANT: BANVILLE, Steve C.; BRATCHER, Shawn R.
APPLICANT: BUFOUR, Gereard E.; COHEN, Howard J.
APPLICANT: DUFOUR, GEREARD E.; COHEN, Howard J.
APPLICANT: JACKSON, Jennifer L.; JONES, Annisa L.
APPLICANT: JACKSON, Jennifer L.; JONES, Annisa L.
APPLICANT: WIGHT, Rachel J.; DANIELS, Susan E.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE PT-1022-1 CIP
CURRENT APPLICATION NUMBER: US/10/378,029
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: equine; OTHER INFORMATION: myoglobin tryptic polypeptide #3
US-10-289-009-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 1.6e-07;
5; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LSEGEWOLVLHVWAKVEADVAGHGQDILIR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LSDGEWQQVLNVWGKVEADIAGHGQEVLIR 31
CURRENT APPLICATION NUMBER: US/10/289,009
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/332,988
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/385,835
PRIOR PLING DATE: 2002-06-03
PRIOR PLING DATE: 2002-06-03
PRIOR PLING DATE: 2002-09-12
PRIOR PLING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-05-31,
PRIOR APPLICATION NUMBER: US 60/147,500
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR PELING DATE: 1999-08-05
PRIOR PELING DATE: 1999-08-05
PRIOR PELING DATE: 1999-08-05
PRIOR PELING DATE: 1999-08-05
PRIOR PELING DATE: 1999-08-05
PRIOR PELING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 60/147,547
PRIOR APPLICATION NUMBER: US 60/147,530
PRIOR APPLICATION NUMBER: US 60/147,530
PRIOR APPLICATION NUMBER: US 60/147,530
PRIOR APPLICATION NUMBER: US 60/147,530
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PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: PCT/US00/15404
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                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 76.7%;
Matches 23; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                       SEQ ID NO 4
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa In David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
                                                                                                                                                                                                                                                                                                                                                    61 LKKHGVTVLTALGAILKKKGHHE---AELKPLAQSHATKHKIPIKYLEFISEAIIHVLHS 117
                                                                                                                                                                                                                                                                                                                                                                                       1 VLSEGEWQLVLHVWAKVEADVACHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED 60
                                                                                                                                                                                                                                                                            14 VLSAADKTNIKNCWGKIGGHGGEYGEBALQRMFAAFPTTKTYFSHIDVSPGSAQVKA---
                                                                                                                                                                                                                                         1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040014087Al 441779.1.j.orfl
US-10-378-029-102
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                                                                                                                             Length 154;
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US-10-424-599-227247
                                                                                                                          Query Match
16.8%; Score 133; DB 15;
Best Local Similarity 26.7%; Pred. No. 1.4e-06;
Matches 40; Conservative 24; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%; Score 132; DB 12; 26.7%; Pred. No. 1.7e-06; cive 24; Mismatches 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26./.
Best A0, Conservative
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Local Similarity
ses 41; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 ---HGKKVADALA---KAADHVEDLPGALSTLSDLHAHKLRVDPVNFKFLSHCLLVTLAC 112
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                                                                                                                                                                                                                                                                                                                                                                                        1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KOZLOV, VLADIMIR
TSYRLOVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
                                                                                                                                                                                                                                                                                                              Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
                                                                                                                                                                                                                                                                                                     16.6%; Score 132; DB 14;
ilarity 26.7%; Pred. No. 1.7e-06;
Conservative 24; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,164
FILING DATE: 23-Apr-2001
CLASSIFICATION AUMBER: US 08/477,668
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/316,424
FILING DATE: 30-SEP-1994
FILING DATE: 30-SEP-1994
FILING DATE: NUMBER: PCT/US94/03349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 RHPGDFGADAQGAMNKALELFRKDIAAKYK 147
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APPLICATION NUMBER: US 08/040,942
FILING DATE: 31-MAR-1993
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                   CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2004-07-27
NUMBER OF SEQ ID NOS: 197
SSCTWARE: PatentIn Ver: 2.1
LENGTH: 142
                                                                                                                                                                                                                                        ; OTHER INFORMATION: Globin, alpha, major US-10-205-219-189
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Patent No. US20020098583A1
GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   TYPE: PRT
ORGANISM: Rattus norvegicus
FILE REFERENCE: WL-A-018200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            40;
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                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL. FOR INHIBITING STEM CELL PROLIFERATION
                                                                                                                                                                                    1 VLSEGEWQLVLHVWAKVEADVAGHGQDILJRLFKSHPETLEKFDRF--KHLKTEAEMKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                         1 VLSGEDKSNIKAAWGKIGGHGAEYGAEALERMFASFPTTKTYFPHFDVSH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 141;
                                                                                                 Length 141;
                                                                                                                                             Indels
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                                                                                            16.1%; Score 128; DB 9; I
llarity 27.0%; Pred. No. 4.6e-06;
Conservative 22; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.1%; Score 128; DB 14;
27.0%; Pred. No. 4.6e-06;
cive 22; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                           116 HSRHPGDFGADAQGAMNKALELFRKDIAAKYK 147
                                                                                                                                                                                                                                                                                                                                                                                                                          110 ASHHPADFTPAVHASLDKFLASVSTVLTSKYR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATA:
APPLICATION NUMBER: US 09/617,840
FILING DATE: 17-JUL-2000
APPLICATION NUMBER: US 09/005,546
FILING DATE: 12-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US94/03349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
APPLICATION NUMBER: US 08/316,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 08/040,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-128-581-24
) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-839-164-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-10-128-581-24
; Sequence 24, Application US/10128581
; Publication No. US20030104984A1
; GENERAL INFORMATION: TREMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-MAR-1993
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 141 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEPHEN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TSYRLOVA, IRENA WOLPE, STEPHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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Best Local Similarity 27.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
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61 KAHGKKVLQSFSDGLKHLDNLKGTFAKLSELHCDQLHVDPENFRLLGNVIVVVLARRLGH 120
                              53 AQVKGHGKKVADALAS----AAGHLDDLPGALSDLHAHKLRVDPVNFKLLSHCLLVTL 109
59 EDLKKHGVTVLTALGAILKKKGHHE---AELKPLAQSHATKHKIPIKYLEFISBAIIHVL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 KKHGVTVLTALGAILKKKGHHBABLKPLAQSHATKHKIPIKYLEFISBAIIHVLHSRHPG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSABEKEAVLGLWGKVNVDEV - - GGEALGRLLVVYPWTQRFFESFGDLSNADAVMGNPKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                        TSYRLOVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
16.0%; Score 127; DB 9;
Best Local Similarity 27.6%; Pred. No. 6.2e-06;
Matches 40; Conservative 20; Mismatches 83;
                                                                                          116 HSRHPGDFGADAQGAMNKALELFRKDIAAKYK 147
                                                                                                                                  110 ASHHPADFTPAVHASLDKFLASVSTVLTSKYR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-SEP-1994
APPLICATION NUMBER: PCT/US94/03349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 08/040,942
FILING DATE: 31-MAR-1993
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/316,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: 1,44 Mb diskette
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DENPDVQAAFOKVVAGVANALAHKY 145
                                                                                                                                                                                                                                             Sequence 8, Application US/09839164 Patent No. US20020098583A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 146 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                      VLADIMIR
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                      APPLICANT: KOZLOV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-128-581-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TSYRLOVA, IRENA
WOLPE, STEPHEN D.
TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS
USEFUL POR INHIBITING STEM CELL PROLIFERATION
                              VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRF--KHLKTEAEMKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%; Score 128; DB 16; Length 141; 27.0%; Pred. No. 4.6e-06; Live 22; Mismatches 73; Indels 10
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                                                                                                                                                                                                          116 HSRHPGDFGADAQGAMNKALELFRKDIAAKYK 147
                                                                                                                                                                                                                                                       110 ASHHPADFTPAVHASLDKFLASVSTVLTSKYR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 MB Disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,699
FILING DATE: 18-Usn-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24 APR 2002
APPLICATION NUMBER: US 09/617,840
FILING DATE: 17-JUL-2000
APPLICATION NUMBER: US 09/005,546
FILING DATE: 12-JNN-1998
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-SEP-1994
APPLICATION NUMBER: PCT/US94/03349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 10/128,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/040,942
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RANDERSSES:
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/316,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPOLOGY: linear
JLE TYPE: peptide
NCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                      59 EDLKKHGVTVLTALGAILKKKGHHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 08
FILING DATE: 31-MAR-1993
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/10463699 Publication No. US20040081640A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 141 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.03
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 1
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Sequence 27, Application US/10128581
Publication No. US20030104984A1
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
WOLPE, STEPHEN D.
TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/617,840
FILING DATE: 17-JUL-2000
APPLICATION NUMBER: US 09/005,546
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
APPLICATION NUMBER: US 08/316,424
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: US 08/316,424
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: PCT/US94/03349
                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSES NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
CITY: ALLINGTON
COUNTRY: U.S.A.
ZUNTRY: U.S.A.
ZUNTRY: U.S.A.
ZURTE: 22201-4714
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION NUMBER: US/10/128,581
FILING DATE: 24-Apr-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 08/040,942
FILING DATE: 31-MAR-1993
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
STRANDEDNESS: «Unknown»;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-128-581-27
                                                                                                                                                                                     NUMBER OF SEQUENCES:
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61 KAHGKKVLQSFSDGLKHLDNLKGTFAKLSELHCDQLHVDPENFRLIGHVIVVVLARRLGH 120
                                                                                                                                          62 KKHGVTVLTALGAILKKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
                                                                     2 LSEGEWOLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL 61
                                                                                                 Gaps
                                         2;
Query Match
Best Local Similarity 27.6%; Pred. No. 6.2e-06;
Matches 40; Conservative 20; Mismatches 83; Indels
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¹²¹ DENPDVQAAFQKVVAGVANALAHKY 145 Dp

Search completed: August 10, 2004, 15:42:27 Job time : 23.2276 secs

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22535, A 23775, A

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence 23678, Sequence 13857, Sequence 22569,

Sequence Sequence

71491, A 20784, A

102870,

Sequence Sequence Sequence

Sequence

Sequence

Scoring table:

Searched:

Database

Perfect score:

Seguence:

protein -

Sequence

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GENERAL INFORMATION:
APPLICANT: Alam, Magsudin
APPLICANT: Alam, Magsudin
TITLE OF INVENTION: HEME PROTEINS HEMAT-HS AND HEMAT-BS AND THEIR USE IN
TITLE OF INVENTION: HEME PROTEINS HEMAT-HS AND HEMAT-BS AND THEIR USE IN
TITLE OF INVENTION: MEDICINE AND MICROSENSORS
FILE REPERENCE: 201040/1038
CURRENT APPLICATION NUMBER: US/09/455,978B
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 76
US-09-455-978B-76
US-09-700-708-4
US-09-701-537-41444
US-09-791-537-41444
US-09-791-537-41444
US-09-791-537-41857
US-09-791-537-21868
US-09-791-537-21885
US-09-791-537-102898
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US-09-791-537-102163
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US-09-791-537-102163
US-09-791-537-21889
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100.0%; Pred. No. 2.4e-77;
iive 0; Mismatches 0;
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US-09-791-537-27073
US-09-791-537-77660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 153; Conservative
      \begin{array}{c} 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 
  US-09-455-978B-76
     \begin{array}{c} 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.75 \\ 7.
                                                                                                                                                                                                     August 10, 2004, 15:26:21; Search time 94.2821 Seconds (without alignments) 1583.930 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                           794
1 VLSEGEWOLVLHVWAKVEAD.....ALELFRKDIAAKYKELGYQG 153
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(ggd2 6/ptodata/2/paa/USO6 COMB.pep:*

(ggd2 6/ptodata/2/paa/USO6 COMB.pep:*

(ggd2 6/ptodata/2/paa/USO6 COMB.pep:*

(ggd2 6/ptodata/2/paa/USO81 COMB.pep:*

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                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length
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67801, A 102163,

Sequence

Sequence 23158, A Sequence 23675, A Sequence 27099, A

Sequence

Sequence 23159, A Sequence 23676, A Sequence 108163,

Sequence 102159,

Sequence 20811, A Sequence 73835, A Sequence 102896,

Sequence 3

Sequence Sequence

151603,

Sequence

Sequence

Sequence Sequence 1

Sequence

Sequence 23089, A Sequence 9291, Ap Sequence 27073, A Sequence 77660, A

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Gaps

0

Indels

Score

Result No.

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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NOWER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 41444
LENGTH: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE REFERENCE: 26/110
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 23678
LENGTH: 154
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                                                                                                                                        61 LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHP 120
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                                                                                                                                                                   62 LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEPISEAIHVLHSRHP 121
                                               1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED 60
                                                                          2 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
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Pred. No. 8.5e-77;
1; Mismatches 0; Indels
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 41444, Application US/09791537; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 23678, Application US/09791537; GENERAL INFORMATION:
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Best Local Similarity 99.3%;
Matches 152; Conservative
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ORGANISM: Physeter catodon
  Matches 153; Conservative
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US-09-791-537-23678
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US-09-791-537-41444
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PAPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARES: Patentin version 3.0
SEQ ID NO 51499
LENGTH: 154
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                                                                                                                         61 LKKHGVTVLTALGAILKKKGHHEAELKPLAOSHATKHKIPIKYLEFISEAIIHVLHSRHP 120
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                                  1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
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APPLICANT: TYAI, Reiko
APPLICANT: TYAI, Reiko
APPLICANT: TOMIOKA, Nobuo
TITLE OF INVENTION Method For Predicting Functions of Protein
TITLE OF INVENTION WUMBER: US/09/700,708
CURRENT APPLICATION NUMBER: US/09/700,708
CURRENT FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: PCT/JP98/02302
PRIOR FILING DATE: 1998-05-26
SOFIWARE: PATENTIN VERSION 3.0
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Pred. No. 2.4e-77;
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; Sequence 51499, Application US/09791537
; GENEAL INFORMATION:
; APPLICANT: Bionomix, Inc.
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US-09-700-708-4
; Sequence 4, Application US/09700708
; GENERAL INFORMATION:
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Best Local Similarity
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US-09-791-537-51499
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LENGTH: 153
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Oseph
APPLICANT: Danzer, Oseph
APPLICANT: Danzer, Oseph
TITLE OF INVENTION: HEREB DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF ED. ID NOS: 153055
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                                                           0; Gaps
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            Score 788; DB 22; Length 154; Pred. No. 1.1e-76;
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                                                      2; Mismatches
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCT
FILLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 23776
LENGTH: 154
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; Sequence 23776, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23088, Application US/09791537 GENERAL INFORMATION:
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SEQ ID NO 23088
LENGTH: 154
         Query Match
Best Local Similarity 98.7%;
Matches 151; Conservative
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Matches 151; Conservative
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US-09-791-537-23088
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; ORGANISM: pdb 2SPO
US-09-791-537-23776
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US-09-791-537-23088
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APPLICANT: Blonomix, Inc.
APPLICANT: Blonomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
SOFTWARE: PALENTIN Version 3.0
SEQ ID NO 13857
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 22569
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                                                                          VLSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
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       Pred. No. 8.5e-77;
1; Mismatches 0; Indels
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; Sequence 22569, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
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GENERAL INFORMATION:
    99.38;
Best Local Similarity 99.3°
Matches 152; Conservative
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CORGANISM: pdb 1CIOA
US-09-791-537-13857
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; ORGANISM: pdb 1MLM
US-09-791-537-22569
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US-09-791-537-13857
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERBNCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 23775
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/10
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARR: Patentin version 3.0
SEQ ID NO 102151
LENGTH: 154
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                                            Score 785; DB 22;
Pred. No. 2.3e-76;
1; Mismatches 1;
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Pred. No. 2.3e-76;
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US-09-791-537-102151
US-09-791-537-22535
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Sequence 102872 Application US/09791537

Sequence 102872 Application US/09791537

Sequence 102872 Application US/09791537

GENERAL INPORMATION:

APPLICANT: Boincent, Inc.

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT PAPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFFWARE: PatentIn version 3.0

SEQ ID NO 102872

LENGTH: 154
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNDER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
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                         Length 154;
                                                                        Indels
                       Score 786; DB 22;
Pred. No. 1.8e-76;
2; Mismatches 0;
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                         99.0%;
98.7%;
                  Query Match
Best Local Similarity 98.74
Matches 151; Conservative
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Matches 151; Conservative
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Pred. No. 3e-76;
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                                                                                        98.7%;
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Best Local Similarity 99.3
Matches 152; Conservative
; TYPE: PRT
; ORGANISM: pdb 1DTWA
US-09-791-537-51498
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNDER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PARENTING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 51498
LENGTH: 153
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 102998
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                                                              Query Match

Best Local Similarity 98.7%;
Matches 151; Conservative
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Best Local Similarity 98.7%;
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US-09-791-537-102151
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Sequence 632, App
Sequence 33346, A
Sequence 33331, A
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Sequence 310, App
Sequence 4103, App
Sequence 7505, App
Sequence 750, App
Sequence 216, App
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Sequence 216, App
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Sequence 226, Appl
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Sequence 201, App
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APPLICANT: Biogen Idec
TITLE OF INVENTION: Surrogate Markers of Pain
FILE REPERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1039
LENGTH: 153

TYPE: PRT ORGANISM: human

; Sequence 1039, Application US/10784004; GENERAL INFORMATION:

US-10-784-004-1039

RESULT 2

DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153

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 Sequence 209, App
Sequence 23358, A
Sequence 8069, Ap
Sequence 10630, Ap
Sequence 11160, A
Sequence 1160, A
Sequence 186, App
Sequence 1558, App
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313, App
16, App
123, Appl
162, Appl
182, App
188, App
1593, Ap
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84.9%; Pred. No. 4.7e-64;
ive 13; Mismatches 10; Indels
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US-10-170-205E-23358
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US-10-170-205E-10630
US-10-170-205E-10630
US-10-170-205E-11160
PCT-USO3-36002-181
US-10-897-005-27
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US-10-897-005-23
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PCT-USO3-36002-162
PCT-USO3-36002-163
US-10-170-205E-34972
PCT-USO3-36002-163
US-10-170-205E-34072
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TITLE OF INVENTION: Surrogate Markers of Pain
FILE REPRENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 632
LENGTH: 153
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Sequence 632, Application US/10784004
GENERAL INFORMATION:
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ORGANISM: human
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Sequence 3331, Application US/10170205E
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN FROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170, 205E
CURRENT PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
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; Pred. No. 1e-58;
18; Mismatches 14; Indels
                      Indels
                      10;
84.9%; Pred. No. 4.7e-64;
tive 13; Mismatches 10
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TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
SUFFER SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
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Matches 120; Conservative
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Matches 129; Conservative
                        Matches 129; Conservative
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US-10-170-205E-33331
      Best Local Similarity
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US-10-170-205E-33331
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Sequence 33330, Application US/10170205E
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEVICES, SUCH AS THEREOF
FILE REPERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ADAMS, MARK
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERRINCE: CLOO1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
SUFFMER FILING DATE: 2002-06-13
SOFTWARE: PATCHIN VERSION 3.2
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                                                Length 153;
                                                                                        10; Indels
                                                88.0%; Score 699; DB 6;
84.9%; Pred. No. 4.7e-64;
                                                                                                                                                                                                                                                                                                     122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                             122 DFGADAQGAMNKALELFRKDMASNYKELGFQG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32946, Application US/10170205E GENERAL INFORMATION:
                                                                                      Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-170-205E-33330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-170-205E-32946
                                                                    Similarity
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US-10-170-205E-33330
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US-10-170-205E-32946
      US-10-784-004-1039
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US-10-793-479-4102
                                                                                                                                                                       Query Match
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                                                         KKHGVTVLTALGAILKKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
                                                                          63 KKHGCTVLTALGTILKKKGQHAABIQPLAQSHATKHKIPVKYLEFISEVIIQVLKKRYSG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
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APPLICANT: Dundert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REPERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/10/793,479
CURRENT FILING DATE: 2004-03-03
PRIOR FILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US/09/513,999
PRIOR FILING DATE: 1999-02-26
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                                                                                                                                                    123 DFGADAQGAMSKALELFRNDIAAKYKELGFQG 154
                                                                                                                               DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
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                                                                                                                                                                                                                                                                                         APPLICANT: Biogen Idec
TITLE OF INVENTION: Surrogate Markers of Pain
TITLE REPERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
SUMBER OF SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
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OTHER INFORMATION: score 3.5
OTHER INFORMATION: seq WQLVLNVWGKVEA/DI
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; GENERAL INFORMATION:
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US-10-784-004-898
Squence 898, Application US/10784004
GENERAL INFORMATION:
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Matches 120; Conservative
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ORGANISM: Homo sapiens
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SEQ ID NO 4103
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Sequence 279565, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yordwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 279565
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.S.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/10/793,479
FILOR APPLICATION NUMBER: US/09/513,999
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36691
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                                                Xaa=Phe or Ile or Leu or Met or Val
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                                                                                                                                                                                                                                                           9; Mismatches
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                                                                                                                                            Xaa=Pro or
                                                                                                                                                                                                                                                           86; Conservative
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NAME/KEY: UNSURE
LOCATION: 84
OTHER INFORMATION: X
FEATURE:
NAME/KEY: UNSURE
LOCATION: 85
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Matches 86; Conserv
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                            OTHER INFORMATION:
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RESULT 12
PCT-US02-17443-214
; Sequence 214, Application PC/TUS0217443
; GENREAL INFORMATION:
; APPLICANT: CuraGen Corporation
; APPLICANT: Agee, Michele
; APPLICANT: Alsobrook, John
; APPLICANT: Alsobrook, John
, POPLICANT: Anderson, David
SOFTWARE: pt_Ft_genes Version 6.0
SEQ ID NO 750
LENGTH: 190
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26.8%;
Best Local Similarity 31.6%;
Matches 49; Conservative 33
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Lepley, Denise
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Casman, Stacie
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Malyankar, Uriel
Miller, Charles
Millet, Isabelle
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Rieger, Daniel
Rothenberg, Mark
Shenoy, Suresh
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DiPippo, Vincent
Edinger, Shlomit
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Smithson, Glennda
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Spytek, Kimberly
Stone, David
Vernet, Corine
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Gorman, Linda
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Gangolli, Esha
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Herrmann, John
Hjalt, Tord
Ji, Weizhen
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                                                                                        ; ORGANISM: Homo sapiens
PCT-US04-07412-750
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                                                                            TYPE: PRT
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PRIOR FILING DATE: 2003-03-14
PRIOR FILING DATE: 2003-03-14
PRIOR FILING DATE: 2002-03-14
PRIOR PLING DATE: 2002-03-14
PRIOR PLING DATE: 2002-03-14
PRIOR PLING DATE: 2002-03-16
PRIOR APPLICATION NUMBER: US 60/340,187
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21-25
PRIOR PLING DATE: 2000-01-21-25
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-25
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FITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 822CIP/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US04/07412
CURRENT FILING DATE: 2004-03-19
                                                                                                                                                              ; LOCATION: -20...1
; OTHER INFORMATION: score 3.5
; OTHER INFORMATION: seq WQLVLNVWGKVEA/DI US-10-793-479-4102
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Goodrich, Ryle W.
Chen, Rui-hong
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Ma, Yunqing
Ghosh, Malabika
Xue, Aidong J.
Asundi, Vinod
Zhao, Qing A.
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APPLICANT: Wang, Jian-rui
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Weng, Gezhi
Wang, Zhiwei
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Ren, Feiyan
                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 KKHGVTVLT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 KKHGATVLT 71
  SOFTWARE: Patent.pm
SEQ ID NO 4102
LENGTH: 71
                                                                                                                                             NAME/KEY: SIGNAL
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                                                                            PRT
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                                                                            TYPE:
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62 KKHGVTVLTALGAILKKKGHHEAE----LKPLAQSHATKHKIPIKYLEFISEAIIHVLH 116
                                                                                                                              19 LSEAERKAVQAMMARLYANCEDVGVAILVRFFVNFPSAKQYFSQFKHMEDPLEMERSPQL 78
                                                                                            2 LSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
                                                 Gaps
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                                               7;
  DB 1; Length 190;
                                               Indels
; Score 212.5; DB 1;
; Pred. No. 5.4e-14;
31; Mismatches 68;
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Padigaru, Muralidhara
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Smithson, Glennda
Spaderna, Steven
Spytek, Kimberly
Stone, David
                                                                      Liu, Xiaohong
Malyankar, Uriel
Miller, Charles
Millet, Isabelle
                                                                                                                                                                                                                                      Patturajan, Meera
                                                                                                                                                                                                                                                               Pena, Carol
Rastelli, Luca
Rieger, Daniel
Rothenberg, Mark
Shenoy, Suresh
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 49; Conserva
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APPLICANT:
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CURRENT FILING DATE: 2002-06-04

PRIOR PAPLICATION NUMBER: 10/160,619

PRIOR APPLICATION NUMBER: 60/295,661

PRIOR APPLICATION NUMBER: 60/295,661

PRIOR APPLICATION NUMBER: 60/295,607

PRIOR FILING DATE: 2001-06-04

PRIOR PLING DATE: 2001-06-04

PRIOR PLING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 60/296,418

PRIOR PLING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 60/296,418

PRIOR PLING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 60/295,575

PRIOR PLING DATE: 2001-06-11

PRIOR PLING DATE: 2001-06-12

PRIOR PLING DATE: 2001-06-12

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PRIOR PLING DATE: 2001-06-14

PRIOR PLING DATE: 2001-06-14

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PRIOR PLING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/297,567

PRIOR PLING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/297,567

PRIOR PLING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/298,285

PRIOR PLING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/297,567

PRIOR APPLICATION NUMBER: 60/298,285

PRIOR PLING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/298,285

PRIOR PLING DATE: 2001-06-14

PRIOR PLING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/298,285

PRIOR PLING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/298,285

PRIOR APPLICATION NUMBER: 60/298,285

PRIOR APPLICATION NUMBER: 60/298,285

PRIOR APPLICATION NUMBER: 60/297,507

PRIOR APPLICATION NUMBER: 60/298,285
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Pred. No. 5.4e-14;
....matches 68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
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APPLICANT: Agee, Michele
APPLICANT: Alesbrook, John
APPLICANT: Anderson, David
APPLICANT: Berghs, Constance
APPLICANT: Burgess, Catherine
APPLICANT: Catterton, Elina
APPLICANT: Catterton, Elina
APPLICANT: DiPippo, Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 31.6%;
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Ellerman, Karen
Gangolli, Esha
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Gorman, Linda
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Herrmann, John
Hjalt, Tord
Ji, Weizhen
Kekuda, Ramesh
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ORGANISM: Homo sapiens
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APPLICANT:
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62 KKHGVTVLTALGAILKKKGHHEAE----LKPLAQSHATKHKIPIKYLEFISEAIIHVLH 116 78 2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL APPLICANT: Scorie, David
APPLICANT: School, Haihong
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-377C-061
CURRENT PAPLICATION NUMBER: PCT/US02/17443
CURRENT PILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR APPLICATION NUMBER: 60/296,414
PRIOR PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,575
PRIOR PLING DATE: 2001-06-01
PRIOR PLING DATE: 2001-06-01
PRIOR PLING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/297,573
PRIOR APPLICATION NUMBER: 60/297,573
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR PLING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR PLING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR PLING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR PLING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 539 SOFTWARE: CuraSeqList version 0.1 26.8%; Score 212.5; DB 1; Length 190; 31.6%; Pred. No. 5.4e-14; 68; Indels 117 SRHPGDFGADAOGAMNKALELFRKDIAAKYKELGY 151 31; Mismatches

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62 KKHGVTVLTALGAILKKKGHHEAE----LKPLAQSHATKHKIPIKYLEFISEAIIHVLH 116
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NUMBER OF SEQ ID NOS: 1920
SOFWARE: pt_FL_genes Version 6.0
SEQ ID NO 750
LENGTH: 190
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PRIOR APPLICATION NUMBER: US 60/365,264
PRIOR PLILOG DATE: 2002-03-14
PRIOR PLILOG DATE: 2002-03-14
PRIOR PLILING DATE: 2001-12-12
PRIOR PLLING DATE: 2000-12-22
PRIOR PLLING DATE: 2000-01-22
PRIOR PLLING DATE: 2000-01-21
PRIOR PLLING DATE: 2000-01-21
PRIOR PLLING DATE: 2000-01-21
PRIOR PLLING DATE: 2000-01-21
PRIOR PLLING DATE: 2000-01-21
PRIOR PLLING DATE: 2000-01-25
PRIOR PLLING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR PLLING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR PLLING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR PLLING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR PLLING DATE: 2000-01-25
PRIOR PLLING DATE: 2000-04-27
PRIOR PLLING DATE: 2000-04-27
PRIOR PLLING DATE: 2000-04-27
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PRIOR PLLING DATE: 2000-04-27
PRIOR PLLING DATE: 2000-04-27
PRIOR PLLING DATE: 2000-04-27
PRIOR PLLING DATE: 2000-04-27
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Sequence 750, Application US/10389559 GENERAL INFORMATION:
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Goodrich, Ryle W.
Chen, Rui-hong
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Best Local Similarity 31.64
Matches 49; Conservative
                                                                                                                                                    Zhou, Ping
Ma, Yunqing
Ghosh, Malabika
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Asundi, Vinod
Zhao, Qing A.
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                                                 Tang, Y. Tom
Wang, Jian-rui
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Ren, Feiyan
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ORGANISM: Homo sapiens
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Wang, Zhiwe
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RESULT 15 US-10-170-205E-19233

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GENERAL INFORMATION:
APPLICANT: ADANS, MATK
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERENCE: CLOO1381
CURRENT APPLICATION WINBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE; Patentin version 3.2
SEQ ID NO 19233
LENGTH: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KKHGVTVLTALGAILKKKGHHEAE----LKPLAOSHATKHKIPIKYLEFISEAIIHVLH 116
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Sequence 19233, Application US/10170205E
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Best Local Similarity 31.6
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Job time: 13.04 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 10, 2004, 15:22:45; Search time 6.66828 Seconds (without alignments) 2207.061 Million cell updates/sec Run on:

Title:

US-09-455-978B-76 794 1 VLSEGEWQLVLHVWAKVEAD.....ALELFRKDIAAKYKELGYQG 153 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mvoglobin [validat		١	•	,	1	1	•	1	1	ı	ı	1	1	1	myoqlobin - Europe	ے	myoglobin - common	i	myoqlobin - potto	١.	ı	1	2			1	ı	ı
SUMMARIES	ID	MYWHP	MYWHW	MYWHC	MYWHH	MYDDAR	MYWHT	MYWHL	MYDD	MYDDBS	MYPE	MYPED	MYWHK	MYWHF	MYWHU	MYWHZ	JN0410	MYHO	MYHOZ	MYCZ	MYLP	MYRB	MYGO	PN0126	MYPG	MYHU	MYMOIM	MYOG	MYGI	MYTS
	DB	-	Н	Н	7	г	Н	Н	Н	-	Н	Н	-	٦	٦	-	~	Н	-	٦	-	Н	П	Н	П	1	Н	н	Н	Н
	Length	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	154	153	153	153	153
oko	Query	100.0	97.4	94.0	93.2	92.9	92.8	92.4	92.3	92.3	92.1	92.1	92.1	91.4		6.06	6.06	89.7	89.7		88.8				88.2	88.0	87.5	87.4	87.3	87.3
	Score	794	773	746	740	738	737	734	733	733	731	731	731	726	725	722	722	712	712	707	705	703	701	701	700	669	695	694	693	693
	Result No.	1	7	3	4	Ŋ	ø	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

100.0%; Score 794; DB 1; Length 153;

Query Match

myoqlobin - siaman	,	1	myoglobin - hanuma	,						myoglobin - slow l					myoglobin - thick-
A61366	MYBAO	MYMORG	MYMOHL	MYMON	MYCJ	MYBTF	MYOT	MYLEM	MYOY	MYLR	MYZC	MYRTNG	MYSLG	MYSLH	MYGC
7	Н	-	-	Н	Н	-1	7	Н	Н	н	Н	_	Н	Н	н
153	153	153	153	153	153	153	153	153	153	153	153	153	153	153	153
87.3	87.0	87.0	87.0	87.0	6.98	6.98	9.98	9.98	86.5	86.3	86.1	86.0	85.9	85.9	85.5
693	691	691	691	691	069	069	688	688	687	685	684	683	682	682	619
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	
MYWHP	
myoglobin (validated) - sperm whale	
C.becass: Pryseter acroam (sperm whale) C.bate: 14-Nov-1983 #semience revision 14-Nov-1983 #foxt chance it.com_2000	
90	
R. Romero-Herrera, A.E., Lehmann, H. Biochim Biochim Biochim 11	
bootman brompys. Acts 33s, 318-32s, 18/4 A;Tttle: Residue 122 of sperm whale and horse myoglobin.	
A Reference number: A90591	
A; Molecule type: protein	
A.Residues: 1-13 <rom></rom>	
R.T.EXPETIMENTAL BOUICE: SKELETAL MUSCLE R.T.RARDO, T.	
iol. 110, 537-568, 1977	
A %Title: Structure of Wygglobin refined at 2.0 angerrom resolution. I. Crystallographic A:Reference number. 309844. MITIN.77144409.	raphic
A; Contents: X-ray crystallography of metmyoglobin, 2.0 angstroms	
A;kestudes: 1-1-20,'A', 1-22-153 <tak> P.Edmindeon b H</tak>	
N. J. C. C. C. C. C. C. C. C. C. C. C. C. C.	
A; Title: Amino-acid sequence of sperm whale myoqlobin.	
A93150	
A;Accession: A93150	
A; Kestudes: 1-12.1, N', 12-153 (-6DM> A: Experimental source: heart muscle	
R.Watson, H.C.; Kendrew, J.C.	
submitted to the Brookhaven Protein Data Bank, April 1973	
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 1-153	
siyinittano, I. siyin brookhassaa Brotaia Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata Brata	
A.Reference number: A50732: PDR:SMRN	
A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 1-153	
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retined at 2.0 angstrom resolution. II. Structure of :77144098; PMID.845960	of deo
A; Contents: annotation; X-ray crystallography of decxymyoglobin, 2.0 angstroms	
A; Description: binds molecular oxygen for intracellular storage and transport, primarily	marily.
C; Keywords: Chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier	
Fi2-147/Domain: globin homology <glb></glb>	
f;e4/Binding Site: oxygen (His) (distal axial ligand) #status experimental F;93/Binding site: heme iron (His) (proximal axial ligand) #status experimental	

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C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000 C;Accession: A90416; A91088; A02500 R;Lehman, L.D.; Dwulet, F.E.; Jones, B.N.; Bogardt Jr., R.A.; Krueckeberg, S.T.; Vissche Biochemistry 17, 3736-3739, 1978 A;Title: Complete amino acid sequence of the major component myoglobin from the humpback A;Reference number: A90416; MUID:79021601; PMID:698193
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A, Residues: 1-60 < EDM>
A, Note: this was the first sequence determined using the modern sequenator
C, Comment: This myoglobin was isolated from skeletal muscle.
C, Superfamily: globin, globin homology
C, Keywords: chromoprotein, heme; iron; metalloprotein; muscle, oxygen carrier
F,2-147/Domain: globin homology < GLB>
F,64/Binding site: oxygen (His) (distal axial ligand) #status predicted
F,93/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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C;Species: Inia geoffrensis (Amazon dolphin)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000
C;Accession: A02503
R;Dwllet, F:E.; Bogardt, R.A.; Jones, B.N.; Lehman, L.D.; Gurd, F.R.N.
Biochemistry 14, 5336-5343, 1975
A;Title: The complete amino acid sequence of the major component myoglobin c
A;Reference number: A02503; MUID: 76062412; PMID:1191640
A;Accession: A02503
A;Nolecule type: protein
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                                                                                                                                                 1 VLSDAEWQLVINIWAKVEADVAGHGQDILIRLFKGHPETLEKFDKFKHLKTEAEMKASED
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A;Residues: 1-153 <LEH>
R;Edman, P.; Begg, G.
Bur. J Biochhem. 1, 80-91, 1967
A,Title: A protein sequenator.
A;Reference number: A91088; MUID:68049168; PMID:6059350
                 Pred. No. 7.8e-55;
6; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myoglobin - humpback whale
C;Species: Megaptera novaeangliae (humpback whale)
                   Best Local Similarity 92.8%;
Matches 142; Conservative
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C;Species: Eschrichtius robustus, Eschrichtius gibbosus (California gray whale)

C;Species: Eschrichtius robustus, Eschrichtius gibbosus (California gray whale)

C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 03-Mar-2000

C;Accession: A02499

R;Bogardt Jr., R.A.; Dwulet, F.E.; Lehman, L.D.; Jones, B.N.; Gurd, F.R.N.

Biochemistry 15, 2597-2602, 1976

A;Title: Complete primary structure of the major component myoglobin of California gray

A;Reference number: A02499; MUD: 76232191; PMID: 938629

A;Residues: A02499; MUD: 76232191; PMID: 938629

A;Residues: 1-153 <BOG>
C;Comment: This myoglobin was isolated from skeletal muscle.
C;Superfamily: globin, globin homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier
F;C-17 Domain: globin homology (GIBS)
F;64/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;64/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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Speciee: Kogia aimus (dwarf sperm whale)
Date: 30-Sep-1993 #squence_revision 30-Sep-1993 #text_change 03-Mar-2000
Accession: A90407; A02506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
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Best Local Similarity 96.7%; Pred. No. 4.6e-57;
Matches 148; Conservative 3; Mismatches 2;
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                            Pred. No. 8.4e-59;
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                                                   Mismatches
100.08; Fig.
                         Best Local Similarity 100.
Matches 153; Conservative
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myoglobin - saddleback dolphin
C;Species: Delphinus delphis (saddleback dolphin)
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Matches 139; Conservative
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Best Local Similarity
Matches 138; Conserv
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C;Species: Globicephala melaena (pilot whale)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000
C;Accession: A02496
R;Jones, B.N.; Dwulet, F.E.; Lehman, L.D.; Garner, M.H.; Bogardt Jr., R.A.; Garner, W.H. Biochemistry 17, 1971-1974, 1978
Biochemistry 17, 1971-1974, 1978
A;Title: Complete amino acid sequence of myoglobin from the pilot whale, Globicephala me A;Reference number: A02496; MUID:78187213; PMID:656376
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C;Species: Orcinus orca (killer whale)
C;Species: Orcinus orca (killer whale)
C;Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text_change 03-Mar-2000
C;Accession: A92255, A90614; A02495
R;Meuth, J.L.; Jones, B.N.; Gurd, F.R.N.
J. Mol. Bvol. 17, 163-166, 1981
A;Ritler Reassignment of residue 122 in the myoglobin from the killer whale, Orcinus orc A;Accession: A92956; MUID:81267443; PMID:6115067
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A;Residues: 1-153 <DWU>
C;Comment: This myoglobin was isolated from skeletal muscle.
C;Superfamily: globin; globin homology
C;Reywords: chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier
F;2-147/Domain: globin homology <GLB>
F;64/Binding site: oxygen (His) (distal avin)
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A/Molecule type: protein
A/Rocession: A02496
A/Molecule type: protein
A/Residues: 1-153 < JON
A/Residues: 1-153 < JON
C/COmment: This myoglobin was isolated from skeletal muscle.
C/Superfamily: globin; globin homology
C/Keywords: Chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier
F/2-14//Domain: globin homology < GLB>
F/64/Binding site: oxygen (His) (distal axial ligand) #status predicted
F/93/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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                                                                                                                                                   2-147/Domain: globin homology <GLB>
64/Binding site: oxygen (His) (distal axial ligand) #status predicted
93/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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Pred. No. 3.6e-54;
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Pred. No. 4.3e-54;
7; Mismatches 5;
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Matches 139; Conservative 7; Mismatches
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Gispeciaes: Tursiops truncatus (bottle-nosed dolphin)
Cispeciaes: No. 1974
Ridones, B.N.; Vigna, R.A.; Dwulet, F.E.; Bogardt, R.A.; Lehman, L.D.; Gurd, F.R.N.
Biochemistry 15, 4418-4422, 1976
A.Filte: Complete amino acid sequence of the myoglobin from the Atlantic bottlenosed dolphin A:Reference number: A02494; MUID:77022063; PMID:974068
A:Reference number: A02494; MUID:77022063; PMID:974068
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A; Molecule type: protein
A; Residues: 1-153 < MBU>
A; Residues: 1-153 < MBU>
B; Castillo, 0.; Lehmann, H; Jones, L.T.
B; Castillo, 0.; Lehmann, H; Jones, L.T.
B; Castillo, 0.; Lehmann, R; 1977
A; Title: The myoglobin of the killer whale (Orcinus orca).
A; Reference number: A90614; MUD: 77134898; PMID: 849459
A; Accession: A90614; MUD: 77134898; PMID: 849459
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
C; Comment: This myoglobin was isolated from skeletal muscle.
C; Superfamily: globin; globin homology
C; Stywords: chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier
F; 2-14/, Domain: globin homology (distal axial ligand) #status predicted
F; 64/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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91.4%; Pred. No. 7.7e-54;
ive 8; Mismatches 5; Indels
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90.8%; Pred. No. 9.3e-54;
iive 9; Mismatches 5.
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myoglobin - Dall's porpoise
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A;Note: the saddleback dolphin is also called Black Sea dolphin
C;Date: 27-Nov-1995 #sequence_revision 31-Mar-1991 #text_change 03-Mar-2000
C;Accession: A&6230; A02497; A3750; A37510; A02444
R;Mang, C.C.; Avila, R.; Jones, B.N.; Gurd, F.R.N.
Biochemistry 16, 4978-4981, 1977
A;Title: Complete primary structure of the major component myoglobin of Pacific common 6
A;Reference number: A26230; MuID:78020893; PMID:911808
A;Accession: A26230
A;Molecule type: protein
A;Residues: 1-153 <WAN>
F;Kluh, I.; Bakardjieva, A.
FRES Lett. 17, 31-34, 197
A;Residues: 1-20, VV,22-27, I',29-31 <KLU>A;Residues: 1-20, VV,22-27, I',29-31 <KLU>A;Residues: 1-20, VV,22-27, I',29-31 <KLU>A;Residues: 1-20, VV,22-27, I',29-31 <KLU>A;Title: Difference in maber: A02497
A;Molecule type: protein
A;Residues: 1-20, VV,22-27, I',29-31 <KLU>A;Title: Difference in amino acid sequence between dolphin and sperm whale myoglobins.
A;Reference number: A37509; MUID:71014229; PMID:5473803
A;Accession: A37509
A;Molecule type: protein
A;Residues: 31-65, D',67-121, O',123-153 <KAR>
A;Note: the amidation states of residues 60, 85, and 132 were not determined and were as R;Nuh: the A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A; He b A
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(c.Species: Phocoena phocoena (harbor porpoise)
(c.Jacession: B92045, A90415; A20498
(c.Jacession: B92045, A90415; A20498
(d.Jacession: B92045, A.; Gurd, F.R.N.
(d. Biol. Chem. 244, 2167-2181, 1969
(d.Jacession: B92045)
(d. Biol. Chem. 245, 2167-2181, 1969
(d. Biol. Chem. 246, 2167-2181, 1969
(d. Biol. Chem. 247, 2167-2181, 1969
(d. Biol. Chem. 247, 2167-2181, 1969
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A;Contents: revision to residue 26
A;Accession: A37510
A;Molecule type: protein
A;Residues: 26 <KL2>
C;Superfamily: globin, globin homology
C;Superfamily: globin, globin homology
F;2-14/VDomain: globin homology (Gills)
F;64/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;93/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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Best Local Similarity 90.89
Matches 138; Conservative
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A; Molecule type: protein
A; Residues: 1-153 < MEU>
C; Superfamily: globin; globin homology
C; Keywords: chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier
F; 2-147 Domain: globin homology < GLB>
F; 2-147 Domain: globin homology < GLB>
F; 447 Domain: globin homology < GLB>
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                                                                                                                 A,Molecule type: protein
A,Residues: 56-90 «MEU
A,Residues: 56-90 «MEU
C,Superfamily: globin, globin homology
C,Keywords: chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier
F;2-147/Donain; globin homology «GLB»
F;2-147/Donain; globin homology «GLB»
F;64/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;93/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000
C;Accession: A02501
K;Lehman, L.D.; Dwulet, F.B.; Bogardt Jr., R.A.; Jones, B.N.; Gurd, F.R.N.
Biochemistry 16, 706-709, 1977
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C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 03-Mar-2000
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 03-Mar-2000
C;Accession: B90415; A02498
R;Meuth, J.L.; Jones, B.N.; Garner, W.H.; Gurd, F.R.N.
B;Intle: J. 3429-3431, 1978
B;Ittle: Complete amino acid sequence of the myoglobin from the Dall porpoishocoena).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 731; DB 1; Length 15:
Pred. No. 1.4e-53;
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A;Reference number: A90415; MUID:79000346; PMID:687594
A;Accession: A90415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
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90.8%; Pred. No. 1...
7; Mismatches
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"Cippecies: Ziphius cavirostris (goose-beaked whale)
Cippecies: Ziphius cavirostris (goose-beaked whale)
Cippecies: Ziphius cavirostris (goose-beaked whale)
Cipate: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 03-Mar-2000
CipAccession: A02504
Elechman, L.D.; Jones, B.N.; Dwulet, F.E.; Bogardt Jr., R.A.; Gurd, F.R.N.
Biochim. Biophys. Acta 625, 221-229, 1980
A;Hitle: Complete amino acid sequence of the major component myoglobin from the goose-be A;Reference number: A02504
A;Reference number: A02504
A;Reference number: A02504
A;Residues: 1-153 < LEH>
Cipperfamily: globin homology
C;Comment: This myoglobin was isolated from skeletal muscle.
C;Comperfamily: globin homology cibs.
C;Comperfamily: globin homology cibs.
C;Comperfamily: globin homology cibs.
F;2-147/Domain: globin homology cibs.
F;2-147/Domain: globin homology cibs.
F;3-147/Domain: globin homology cibs.
                                                        A.Title: Complete amino acid sequence of the major component myoglobin from Hubb's beake A;Reference number: A02505; MUID:81000592; PMID:7407230
A;Accession: A02505
A;Accession: A02505
A;Accession: A02505
A;Accession: A02505
C;Comment: Type: protein
A;Residues: 1-153 < DWU>
C;Comment: This myoglobin was isolated from skeletal muscle.
C;Superfamily: globin, peme; iron; metalloprotein; muscle; oxygen carrier
C;Ceywords: chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier
F;2-147/Domain: globin homology cGibs
F;2-147/Domain: globin homology cGibs
F;6-1851Binding site: oxygen (His) (distal axial ligand) #status predicted
F;93/Binding site: heme iron (His) (proximal axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 153;
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90.1%; Pred. No. 7.6e-53;
iive 7; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
91.3%; Score 725; DB
Best Local Similarity 90.1%; Pred. No. 4.3e
Matches 137; Conservative 8; Mismatches
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Job time : 7.66828 secs
                                   Biophys. Acta 624, 121-129,
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Best Local Similarity 90.1
Matches 137; Conservative
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C;Species: Balaenoptera physalus (finback whale, common rorqual)
C;Date: 27-Nov-1965 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000
C;Accession: A02502
R;DiMarchi, R.D.; Wang, C.C.; Hemenway, J.B.; Gurd, F.R.N.
Biochamistry 17, 1968-1970, 1978
Biochamistry 17, 1968-1970, 1978
A;Title: Complete amino acid sequence of the major component myoglobin of finback whale A;Reference number: A02502; MUID:78187212; PMID:656375
A;Accession: A02502
A;Accession: A02502
A;Residues: 1-153 *DIM>
C;Comment: This myoglobin was isolated from skeletal muscle.
C;Comment: This myoglobin homology
C;Comment: This myoglobin homology
C;Superfamily: globin, peme; iron; metalloprotein; muscle; oxygen carrier
F;2-147/bomain: globin homology c;CiBs
F;2-147/bomain: globin homology c;CiBs
F;64/Rinding site: oxygen (His) (distal axial ligand) #status predicted
F;93/Binding site: heme iron (His) (proximal axial ligand) #status predicted
A;Title: The complete amino acid sequence of the major component myoglobin from the Arct A;Reference number: A02501; MUID:77112438; PMID:836810
A;Recession: A02501
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-153 < LEH>
C;Comment: This myoglobin was isolated from skeletal muscle.
C;Comment: This myoglobin was isolated from skeletal muscle.
C;Comment: This myoglobin pownology
C;Reywords: chromoprotein; heme; iron; metalloprotein; muscle; oxygen carrier
F;2-147/Domain: globin homology <GLD>
F;2-147/Domain: globin homology <GLD>
F;64/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;93/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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C;Species: Mesoplodon carlhubbsi (Hubbs' whale)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000
C;Accession: A03505
R;Dwulet, J.A.; Dwulet, F.E.; Gurd, F.R.N.
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92.1%; Score 731; DB 1; Length 153;
Best Local Similarity 90.8%; Pred. No. 1.4e-53;
Matches 139; Conservative 7; Mismatches 7; Indels
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

August 10, 2004, 15:19:00 ; Search time 4.81598 Seconds (without alignments) 1654.229 Million cell updates/sec Run on:

US-09-455-978B-76

Perfect score: Title:

1 VLSEGEWQLVLHVWAKVEAD......ALELFRKDIAAKYKELGYQG 153 Sequence:

141681 segs, 52070155 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

141681 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB a Maximum DB a

Post-processing: Minimum Match 0% Maximum Match 100%

Database :

SwissProt 42:*

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	02185 physete	4	7	P02178 megaptera n	31	P02174 globicephal	73	2			0	P02183 mesoplodon	9	P02182 ziphius cav		P02145 pan troglod		0	gorilla	8 ondatra	9 sus scro	4	0	8	9	tupai	51 actus	-#	P02152 callithrix	53	169	113	P02164 orycteropus
SUMMARIES		ID	PHY		MYG_ESCGI	MYG MEGNO	MYG_INIGE						MYG_BALPH	MYG MESCA		MYG_ZIPCA	MYG_HORSE	MYG_PANTR	MYG_PERPO	MYG_RABIT	MYG GORBE	MYG_ONDZI	MYG_PIG	MYG_HUMAN	MYG_MACFA	MYG_PONPY	MYG_HYLAG		MYG_AOTTR			MYG_ROUAE	MYG_LEPMU		MYG_ORYAF
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ð		Match	100.0	97.4	94.0	93.2	92.9	95.8	92.4	92.3	92.1	92.1	91.4	91.3	6.06	6.06	90.3	89.0	88.8	88.5	88.3	88.3	88.2	88.0	87.5	87.4	87.3	87.3	87.0	87.0	86.9	86.9	9.98	86.6	86.5
		Score	794	773	746	740	738	737	734	733	731	731	726	725	722	722	717	707	705	703	701	701	200	669	695	694	693	693	691	691	069	069	688	688	687
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	1 zalophus ca	6 ctenodactyl	2 halichoerus	2 delphinapte	8 galago cras	3 cebus apell	4 lagothrix l	1 ochotona pr	8 spalax leuc	1 cervus elap	
P0216	P02161	P2085	P0216	P83683	P0216	P0215	P0215	P0217	P04248	P02191	P04249
MYG NYCCO	MYG_ZALCA	MYG CTEGU	MYG_HALGR	MYG_DELLE	MYG GALCR	MYG CEBAP	MYG_LAGLA	MYG_OCHPR	MYG_SPAEH	MYG CEREL	MYG_PROGU
Н	Т	Н	Н	٦	Н	н	Н	Н	Н	Н	П
153	153	153	153	153	153	153	153	153	153	153	153
86.3	86.1	86.0	85.9	85.6	85.5	85.4	85.4	85.4	85.3	84.9	84.9
	84	683	682	680	619	678	678	678	677	674	674
685	9										

ALIGNMENTS

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II. Structure of
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Lionetti C., Guanziroli M.G., Frigerio F., Ascenzi P., Bolognesi M.;
"X-ray crystal structure of the ferric sperm whale myoglobin:
imidazole complex at 2.0-A resolution.";
J. Mol. Biol. 217:409-412(1991).
                                                                                                                                                                                                                                                                                            Physeter catodon (Sperm whale) (Physeter macrocephalus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
Physeteridae; Physeter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takano T.;
"Structure of myoglobin refined at 2.0-A resolution. I.
Crystallographic refinement of metmyoglobin from sperm whale.";
J. Mol. Biol. 110:537-568(1977).
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MEDLINE=77144097; PubMed=845959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of myoglobin refined at 2.0-A resolution. deoxymyoglobin from sperm whale."; J. Mol. Biol. 110:569-584(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Romero-Herrera A.E., Lehmann H.;
"Residue 122 of sperm whale and horse myoglobin.";
Biochim. Biophys. Acta 336:318-323(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edmundson A.B.;
"Amino-acid sequence of sperm whale myoglobin.";
Nature 205:883-887(1965).
                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                       153 AA
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MEDLINE=99158603; PubMed=10049310;
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Phillips S.E.V.;
                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
TISSUE=Heart muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISION TO 122,
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                                                                                                                                                                                                                                             Myoglobin.
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1LZK, 21-AUG-02.
1JJR1, 23-JAUG-96.
1MBC, 27-OCT-83.
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10FJ;
10FK;
1SPE;
1SWM;
1TES;
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### X-RAY CRYSTALLOGARAPHY (1.4 ANGSTROMS).

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Brunori M., Cutruzzola F., Savino C., Travaglini-Allocatelli C., Vallone B., Gibson Q.H.;
"Structural dynamics of ligand diffusion in the protein matrix:
strudy on a new myoglobin mutant Y(Bl0) Q(E7) R(Bl0).";
Biophys. J. 76:1259-1269(1999).
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08 - MAR - 96 . 31 JAN - 94 . 31 JAN - 94 . 31 JAN - 94 . 31 JAN - 94 . 31 JAN - 96 . 31 JAN - 94 . 31 JAN - 94 . 31 JAN - 94 . 31 JAN - 94 . 31 JAN - 94 .

31-JAN-94. 31-JAN-94. 31-JUL-94. 31-JUL-94. 31-JUL-94.

Query Match

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61 LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                    oxygen and facilitates the
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                                                                                                                              Eschrichtius gibbosus (California gray whale) (Eschrichtius robustus).
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                                                                                                                                                                                                                                                                                 TISSUE=Skeletal muscle;
MEDLINE=76232191; PubMed=938629;
Bogardt R.A. Jr., Dwulet F.E., Lehman L.D., Jones B.N., Gurd F.R.N.;
"Complete primary structure of the major component myoglobin of
California gray whale (Eschrichtius gibbosus).";
Biochemistry 15:2597-2602(1976).
-I- FUNCTION: Serves as a reserve supply of oxygen and facilitates th
movement of oxygen within muscles.
-I- SIMILARITY: Belongs to the globin family.
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Lehman L.D., Dwulet F.E., Jones B.N., Bogardt R.A. Jr.,
Krueckeberg S.T., Visscher R.B., Gurd F.R.N.;
"Complete amino acid sequence of the major component myoglobin from
the humpback whale, Megaptera novaeangliae.";
                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti,
Eschrichtiidae, Eschrichtius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Cetacea, Mysticeti;
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92.8%; Pred. No. 1.6e-57;
ive 6; Mismatches 5; Indels
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METAL 64 F4 TRON (HEME DISTAL LIGAND).
METAL 93 93 IRON (HEME PROXIMAL LIGAND).
SEQUENCE 153 AA; 17118 MW; 4A5587BADE805C7D CRC64;
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                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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HSSP; P02185; 1BZ6.
InterPro; IPR000971; Globin.
Pfam; PF00042; Globin; PRMTS; PR00612; Globin; 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
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nes 142, Conservative
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                                                                                                                                                                                                                       NCBI_TaxID=9764;
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                                                                                                                                                                                                                                                                 SEQUENCE
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A Dwulet F.E., Jones B.N., Lethman L.D., Gurd F.R.N.;

Dwulet F.E., Jones B.N., Lethman L.D., Gurd F.R.N.;

Dwulet F.E., Jones B.N., Lethman L.D., Gurd F.R.N.;

The complete amino acid sequence of the major component myoglobin of dwarf sperm whalf a final simus).";

Biochemistry 16:873-877(1977).

-1- FUNCTION: Serves as a reserve supply of oxygen and facilitates the movement of oxygen within muscles.

-1- FUNCTION: Serves may a reserve supply of oxygen and facilitates the movement of oxygen within muscles.

-1- SIMILARITY: Belongs to the globin family.

PIR; A99407; MYMHW.

InterPro; IPR00037; Globin.

R Flan; PR00613; MYOGLOBIN.

R PRINTS; PR00613; MYOGLOBIN.

R PROSITE: PS01033; GLOBIN; 1.
                                                             ö
                                                                                                                                                                                         61 LKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHP 120
                                                                                                                                                                                                                     61 LKKGGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEPISEAIIHVLHSRHP 120
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                                                                                                                                     1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
                                                                                                     1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
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                                                             Gaps
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Mammalia, Eutheria, Cetartiodactyla, Cetacea, Odontoceti,
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0
                  Length 153;
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96.7%; Pred. No. 7.5e-60;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heme; Oxygen transport; Transport; Muscle.

METAL 64 64 IRON (HEME DISTAL LIGAND).

METAL 93 93 IRON (HEME PROXIMAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5771A432C7B32614 CRC64;
                                                             0;
                100.0%; Score 794; DB 1; 100.0%; Pred. No. 1.2e-61;
                                                                                                                                                                                                                                                                                 GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                        GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        153 AA
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                                                         0; Mismatches
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                                    Best Local Similarity 100.
Matches 153; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Physeteridae; Kogia.
NCBI_TaxID=9752;
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NCBI_TaxID=9731;
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                      61 LKKHGNIVLTALGGILKKKGHHEAELKPLAOSHATKHKIPIKYLEFISDAIIHVLHSRHP 120
                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                       1 VLSDAEWQLVLNIWAKVEADVAGHGQDILIRLFKGHPETLEKFDKFKHLKTEAEMKASED 60
                                          Edman P., Begg G.,
"A protein sequenator.";
Eur. J. Blochem. 1:80-91(1967).
-!- FUNCTION: Serves as a reserve supply of oxygen and facilitates the movement of oxygen within muscles.
-!- MISCELLANBOUS: This sequence was the first determined using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dwulet F.E., Bogardt R.A., Jones B.N., Lehman L.D., Gurd F.R.N.;
"The complete amino acid sequence of the major component myoglobin of
Amazon river dolphin (Inia geoffrensis).",
Biochemistry 14:5336-5343(1975).
-!- FUNCTION: Serves as a reserve supply of oxygen and facilitates the
movement of oxygen within muscles.
-!- SIMILARITY: Belongs to the globin family.
                                                                                                                                                                                                                                                                                                                                         1 VLSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inia geoffrensis (Amazon dolphin).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Odontoceti, Iniidae,
                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                         Length 153;
                                                                                                                                                                                                                                                                                        93.2%; Score 740; DB 1; Length 15
92.2%; Pred. No. 5.2e-57;
ive 6; Mismatches 6; Indels
                                                                                                                                                                                        Print, Product; globin; 1.
PRINTS; PRO0613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
Heme; Oxygen transport; Transport; Muscle.
METAL 93 93 IRON (HEME DISTAL LIGAND).
SEQUENCE 153 AA; 17132 MW; 4FAFDBIADEB05C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ADFGADAQAAMNKALELFRKDIAAKYKELGFQG 153
                                                                                                                 Edman sequencing system.
-!-SIMILARITY: Belongs to the globin family.
PIR, 409416, MVHH.
HASP: P02185; 1BZ6.
InterPro; IPR000971; Globin.
InterPro; IPR002335; Mygglobin.
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Last annotation update)
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                                   MEDLINE=68049168; PubMed=6059350;
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HSSP, P02188; 1WHA.
InterPro; IPR000931; Globin.
InterPro; IPR000335; Myoglobin.
PRIM; PR00042; Globin; 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
Biochemistry 17:3736-3739(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 01, Created)
(Rel. 01, Last seq
(Rel. 41, Last ann
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nes 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Skeletal muscle;
                        SEQUENCE OF 1-60.
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28-FEB-2003
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P02181;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Odontoceti, Delphinidae,
                                                                                                                                                                                                                  2 LSDGEWQLVLNIWGKVEADLAGHGQDVLIRLFKGHPETLEKFDKFKHLKTEAEMKASEDL
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                                                                                                                                                                                          2 LSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
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                                                                                                                                                  Gaps
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MEDLINE-78187213; PubMed-656376;
Jones B.N., Dwulter F.E., Lehman L.D., Garner M.H., Bogardt R.A.
Garner W.H., Gurd F.R.N.;
"Complete amino acid sequence of myoglobin from the pilot whale,
                                                                                                                                                  .,
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                                                                                                     Length 153;
                                                                                                   92.9%; Score 738; DB 1; Length 15
91.4%; Pred. No. 7.7e-57;
ive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.8%; Score 737; DB 1; Length 15
92.1%; Pred. No. 9.4e-57;
ive 7; Mismatches 5; Indels
Heme; Oxygen transport; Transport; Muscle.

METAL 64 64 IRON (HEME DISTAL LIGAND).

METAL 93 93 IRON (HEME PROXIMAL LIGAND)
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2 LSDGEWQLVLNVWGKVEADLAGHGQDVLIRLFKGHPETLEKFDKFKHLKTEADMKASEDL 61
                                        Tursiops truncatus (Atlantic bottle-nosed dolphin), and Delphinus delphis (Saddleback dolphin) (Black sea dolphin). Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Serves as a reserve supply of oxygen and facilitates the
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MEDLINE=71014229; PubMed=5473803;
Karadjova M., Nedkov P., Bakardjieva A., Genov N.;
"Differences in amino acid sequence between dolphin and sperm whale
                                                                                                                                                                                                                                                                myoglobin from the Atlantic
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=78020893; PubMed=911808; Mang C.-C., Avila R., Jones B.N., Gurd F.R.N.; Mang C.-C., Avila R., Jones B.N., Gurd F.R.N.; Complete primary structure of the major component myoglobin of Pacific common dolphin (Delphinus delphis)."; Biochemistry 16:4978-4981(1977).
                                                                                                                                                                                       SPECIES-T.truncatus; TISSUE-Skeletal muscle;
MEDLINE-77022063; PubMed-974068;
Jones B.N., Vigna R.A., Dwulet F.E., Bogardt R.A., Lehman L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kluh I., Bakardjieva A.; "Primary structure of N-terminal part of molecule of dolphin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heme; Oxygen transport; Transport; Muscle.
METAL 64 64 IRON (HEME DISTAL LIGAND).
METAL 93 93 IRON (HEME PROXIMAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A408C4895BB5AC53 CRC64;
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V -> I (IN REF. 3).
N -> D (IN REF. 4).
E -> Q (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 733; DB 1;
Pred. No. 2.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  movement of oxygen within muscles.
-!- SIMILARITY: Belongs to the globin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                           SPECIES=D.delphis; TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1977) to the PIR data bank
                                                                                                                                                                                                                                                             "Complete amino acid sequence of the myog
bottlenosed dolphin, Tursiops truncatus."
Biochemistry 15:4418-4422(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iochim. Biophys. Acta 221:136-139(1970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.3%; Score 733;
90.8%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A02494; MYDD.
PIR; A26230; MYDDBS.
HSSP; P02185; 1BZ6.
InterPro; IPR000971; Globin.
InterPro; IPR002335; Myoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 IR
93 IR
21 L
28 V
66 N
122 E
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PRINTS, PR00613, MYOGLOBIN.
PROSITE, PS01033, GLOBIN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myoglobin.";
FEBS Lett. 17:31-34(1971).
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                                                                                                                               NCBI_TaxID=9739, 9728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=D. delphis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 31-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=D.delphis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-31
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                                                                                                                                                                                                                                                 Gurd F.R.N.;
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     Myoglobin.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
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CONFLICT
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Best Local (
                                                                                                                   Fursiops
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Exteletal muscle,
MEDLINE-77134898; PubMed=849459;
Castillo O., Lehmann H., Jones L.T.;
The myoglobin of the killer whale (Orcinus orca).";
Biochim. Biophys. Acta 491:23-28(1977)
-: FUNCTION: Serves as a reserve supply of oxygen and facilitates the
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skeletal muscle;
MEDLINE=81257443, PubMed=6115067;
MEUTINE=81257443, PubMed=6115067;
MEUTH J.L., Jones B.N., Gurd F.R.N.;
"Reassignment of residue 122 in the myoglobin from the killer whale,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.4%; Score 734; DB 1; Length 153; 91.4%; Pred. No. 1.7e-56; Indels s; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; Pruces, Process, MYOGLUCE..., PRINTS; PROS613; MYOGLUCE..., PROSITE: PROJ033; GLOBIN; 1.
Heme; Oxygen transport; Transport; Muscle.
Heme; Oxygen transport; Transport; Muscle.
METAL 64 64 IRON (HEME DISTAL LIGAND).
METAL 93 120 (IN REF. 2).
17071 MW; A408C49BCBB83C4C CRC64;
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movement of oxygen within muscles.
-!- SIMILARITY: Belongs to the globin family.
BIR; A92956; MYWHL.
INTERPROPERS; 1A6M.
INTERPROPERS; 1A6M.
INTERPROPERTY: Globin.
INTERPROPERTY: Myoglobin.
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                                                                                                                                                                      (Rel. 01, Last sequence update) (Rel. 40, Last annotation update)
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Last annotation update)
                                                                                                                153 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orcinus orca.";
J. Mol. Evol. 17:163-166(1981).
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(Rel. 01, Last seq. (Rel. 40, Last ann
                                                                                                                                                    (Rel. 01, Created)
                                                                                                                                                                                                                                             Orcinus orca (Killer whale).
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Matches 139; Conservative
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P02172; P02175;
21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9733;
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16-OCT-2001
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P02173;
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RESULT 8 MYG_TURTR

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            62 KKHGNIVLTALGAILKKKGHHDAELKPLAQSHATKHKIPIKYLEFISEAIHVLHSRHPA 121
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KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
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                                                                                                                                                                                                                                                                            MEDLINE=77112438; PubMed=836810; Lehman L.D., Dwulet F.E., Bogardt R.A. Jr., Jones B.N., Gurd F.R.N.; Lehman L.D., Dwulet F.E., Bogardt R.A. Jr., Jones B.N., Gurd F.R.N.; "The complete amino acid sequence of the major component myoglobin from the arctic minke whale, Balaenoptera acutorostrata."; Biochemistry 16:706-709(1977).

-I. FUNCTION: Serves as a reserve supply of oxygen and facilitates the movement of oxygen within muscles.

-I. SIMILARITY: Belongs to the globin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                         Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Sukaryota; Metazota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 153;
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90.8%; Pred. No. 3.1e-56;
"**ematches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO1035; GAUGHAN, A.
Heme; Oxygen transport; Transport; Muscle.
METAL 64 EA IRON (HEME DISTAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17155 MW; A5364E71B9705C6E CRC64;
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                                                      EFGADAQGAMNKALELFRKDIAAKYKELGFHG 153
                                         DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                      (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 40, Last annotation update)
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(Rel. 01, Last sequence update)
(Rel. 40, Last annotation update)
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HSSP: POD185; IBZ6.
InterPro; IPR000971; Globin.
InterPro; IPR002335; Myoglobin.
Pram; PF00042; globin; 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                      TISSUE=Skeletal muscle;
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Matches 139; Conserv
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21-JUL-1986
16-OCT-2001
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21-JUL-1986
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P02176;
                                                                                                                                                                       Myoglobin.
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                                                                                                                  MYG BALAC
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MYG PHOPH
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KKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPG 121
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Phocoenoides dalli dalli (Dall's porpoise).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Phocoenidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Serves as a reserve supply of oxygen and facilitates the movement of oxygen within muscles.
-!- SIMILARITY: Belongs to the globin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=P.phocoena, and P.d.dalli;
MEDLINE=79000346; PubMed=687594;
Meuth J.L., Jones B.N., Garner W.H., Gurd F.R.N.;
"Complete amino acid sequence of the myoglobin from the Dall porpoise (Phocoenoides dalli dalli) and reinvestigation of the primary structure of the myoglobin from common porpoise (Phocoena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti;
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                                                                                                                                                                                                                                                                                        porpoise, and sperm
of harbor seal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.1%; Score 731; DB 1; Length 153; 90.8%; Pred. No. 3.1e-56; ive 7; Mismatches 7; Indels
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METAL 64 64 IRON (HEME DISTAL LIGAND).
METAL 93 93 IRON (HEME PROXIMAL LIGANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 AA; 17101 MW; 3FA2F4561A35CC2E CRC64;
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Last annotation update)
                                                                                                                                                                                                SPECIES=P.phocoena;
MEDLINE=69177451; PubMed=5782005;
Bradshaw R.A., Gurd F.R.N.;
"Comparison of myoglobins from harbor seal,;
whale. V. The complete amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, AND REVISIONS TO 83 AND 85.
                                                                                                                                                                                                                                                                                                                                         porpoise myoglobins.";
J. Biol. Chem. 244:2167-2181(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P02185, 1EZ6.
InterPro; IPR000971; Globin.
InterPro; IPR002315; My0globin.
Pfam, PP00042; globin; I.
PRINTS; PR00613; MY0GLOBIN.
PROSITE; PS01033; GLOBIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phocoena).";
Biochemistry 17:3429-3431(1978).
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. 01, Last sequed. 40, Last anno
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NCBI_TaxID=9770;
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Matches 138; Conservative
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                                                                                                                 NCBI_TaxID=9742, 9745;
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PIR; B92045; MYPE.
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21-JUL-1986
16-OCT-2001
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P02180;
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PRT;
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InterPro; IPR002335; Myoglobin.
Pfam; PF00042; Globin. 1.
PRIMTS; PR0613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                            Castor fiber (Eurasian beaver).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sukhomlinov B.F., Drobot L.B.;
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                                                        Matches 137; Conservative
                                                                                                                                                                                                                                                                                             STANDARD;
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HSSP; P02189; 1MWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                           Similarity
                                                                                                                                                                                                                                                                                             MYG_CASFI
P14396;
                                                                                                                                                                                                                                                                                                                                                               Myoglobin.
  SEQUENCE
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                              Query Match
                                            Best Local
                                                                                                                                                                                                                                                                 RESULT 13
MYG CASFI
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MEDLINE=81000592; PubMed=7407230;

MEDLINE=81000592; PubMed=7407230;

MEDLINE=81000592; PubMed=7407230;

T "Complete amino acid sequence of the major component myoglobin from recomplete amino acid sequence of the major component myoglobin from this beaked whale, Mesoplodon carlhubbsi.";

Biochim. Biophys. Acta 624:121-129(1980).

I-FUNCTION: Serves as a reserve supply of oxygen and facilitates the movement of oxygen within muscles.

I-SIMILARITY: Belongs to the globin family.

PIR, AO2505; MYMHU.

PRESP: P02185; 1A6M.

InterPro; IPR002375; Myoglobin.

RIGEPRO; IPR002375; Myoglobin.

PRESP: P001042; Globin, 1.

PRESP: P001042; Globin, 1.

PRESP: P001042; Globin, 1.

PRESP: P001042; Globin, 1.

PRESP: P001042; GLOBIN.
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                                                       finback whale (Balaenoptera physalus).";
Biochemistry 17:1968-1970(1978).
-!- FUNCTION: Serves as a reserve supply of oxygen and facilitates the
                                                                                                                                                                                                                                                                                                                                                                 1 VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASED
                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Odontoceti, Ziphiidae,
                           Dimarchi R.D., Wang C.-C., Hemenway J.B., Gurd F.R.N.; "Complete amino acid sequence of the major component myoglobin of
                                                                                                                                                                                                                                                                                          Score 726; DB 1; Length 153;
Pred. No. 8.4e-56;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                    IRON (HEME DISTAL LIGAND).
IRON (HEME PROXIMAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heme; Oxygen transport; Transport; Muscle.

METAL 64 64 IRON (HEME DISTAL LIGAND).

METAL 93 93 IRON (HEME PROXIMAL LIGAND).
                                                                                                                                                                                                                                                                 8AFC89C1BF00291F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01, Last sequence update)
40, Last annotation update)
                                                                                            movement of oxygen within muscles.
-!- SIMILARITY: Belongs to the globin family.
PIR, A02502, MYWHF.
HSSP; P02185; 1BZ6.
InterPro, IPR000971; Globin.
InterPro, IPR002335; Myoglobin.
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                                                                                                                                                                                                                          Heme; Oxygen transport; Transport; Muscle.
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TISSUE=Skeletal muscle;
MEDLINE=78187212; PubMed=656375;
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01, Last sequ
                                                                                                                                                                                                                                                                 153 AA; 17086 MW;
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90.2%;
                                                                                                                                                                             Pfam, PF00042; globin, 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
                                                                                                                                                                                                                                                                                                        Best Local Similarity 90.2
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Skeletal muscle;
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(Rel.
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MYG MESCA
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-1. FUNCTION: Serves as a reserve supply of oxygen and facilitates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL
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                                                                                                            Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Castoridae; Castor.
NCBI_TaxID=10185;
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Pred. No. 1.8e-55;
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METAL 64 FRON (HEME DISTAL LIGAND).
METAL 63 93 93 PRON (HEME PROXIMAL LIGAND).
SEQUENCE 153 AA; 17020 MW; 4FD93C4E116B6D4D CRC64;
                                                                                                            7; Indels
153 AA; 17136 MW; 8BA3DB535CBE91E9 CRC64;
                                                   91.3%; Score 725; DB 1; 90.1%; Pred. No. 1e-55;
                                                                                                                                                                                                                                                                                                                                                                              122 DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
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01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 AA
                                                                                                         8; Mismatches
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SPECIES=Horse;
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PIR;
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PDB;
PDB;
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Lehman L.D., Jones B.N., Dwulet F.E., Bogardt R.A. Jr., Gurd F.R.N.;
Lehman L.D., Jones B.N., Dwulet F.E., Bogardt R.A. Jr., Gurd F.R.N.;
"Complete amino acid sequence of the major component myoglobin from
the goose-beaked whale. Ziphius cavirostris.";
Biochim. Biophys. Acta 625:221-229(1980).
-!-FUNCTION: Serves as a reserve supply of oxygen and facilitates the
movement of oxygen within muscles.
-!-SIMILARITY: Belongs to the globin family.
PIR: A02504; MYWHZ.
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                                                                                                                                          Ziphius cavirostris (Goose-beaked whale).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Equus caballus (Horse), and
Equus burchelli (Plains zebra) (Equus quagga).
Equus burchelli (Plains zebra) (Equus quagga).
Butaryota; Metacoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796, 9790;
                                                                                                                                                                                                                                                                                                                                                                                                                            A PIR; ACISON, MIN...

R HSSP; P02185; LA6M.

R HSSP; P02185; LA6M.

A InterPro; IPR000971; Globin.

DR Fram; Pr00613; Globin; 1.

DR PRINTS; PR00613; MYOGLOBIN; 1.

DR PRINTS; PR00103; GLOBIN; 1.

DR PROSITE; PS01033; GLOBIN; 1.

Heme; Oxygen transport; Transport; Muscle.

64 64 IRON (HEME DISTAL LIGAND).

9 1 RON (HEME DISTAL LIGAND).

9 1 RON (HEME DISTAL LIGAND).

9 1 RON (HEME DISTAL LIGAND).

9 1 RON (HEME DISTAL LIGAND).
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90.1%; Pred. No. 1.8e-55;
ive 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=7006402; PubMed-4902609;
Dautrevaux M., Boulanger Y., Han K., Biserte G.;
"Covalent structure of horse myoglobin.";
Eur. J. Biochem. 11:267-277(1969).
                                      (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 40, Last annotation update)
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
  153 AA
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 90.1
Matches 137; Conservative
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  STANDARD;
                                                                                                                                                                                                                            NCBI_TaxID=9760;
                                                           21-JUL-1986
16-OCT-2001
                                        21-JUL-1986
MYG_ZIPCA
P02182;
                                                                                                    Myoglobin.
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P02188;
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                                                                                                                                                                                                             Ziphius
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MYG_HORSE
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"Structure of a ligand-binding intermediate in wild-type carbonmonoxy myoglobin.", Nature 403:921-923(2000).

-!- FUNCTION: Serves as a reserve supply of oxygen and facilitates the
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                                                                                                                                                                                               MEDLINE=90147691, PubMed=2302197,
Jahnen W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;
Jahnen W., Ward in D., Reid G.E., Moritz R.L., Simpson R.J.;
Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage in polyacrylamide gels.";
Biochem. Biophys. Res. Commun. 166:139-145(1990).
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MEDLINE=9538313; PubMed=7654702;
Bogumil R., Maurus R., Hildebrand D.P., Brayer G.D., Mauk A.G.;
"Origin of the pH-dependent spectroscopic properties of
pentacoordinate metunyoglobin variants.";
Biochemistry 34:10483-10490(1995).
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"Horse heart metmyoglobin. A 2.8-A resolution three-dimensional
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SPECIES-Horse; TISSUE-Skeletal muscle;
Romero-Herrera A.E., Lehmann H.;
"Residue 122 of sperm whale and horse myoglobin.";
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SIMILARITY: Belongs to the globin family.
# 490603; MYHOZ.
# A91098; MYHO.
                                                                                                                                                                                                                                                                                                                                                                               COMPOSITION OF TRYPTIC AND PEPTIC PEPTIDES
                                                                                         Biochim. Biophys. Acta 336:318-323(1974)
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J. Biol. Chem. 263:4263-4268(1988)
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MEDLINE=88153746; PubMed=3346247;
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1RSE, 23-DEC-96.
1XCH, 17-SEP-97.
1WLA, 14-JAN-98.
1AZI, 25-FEB-98.
1DWR, 03-MAR-00.
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DR PFam; PR00042; Globin.
DR PROSITE; PR00613; MYOGLOBIN.
DR PROSITE; PR00613; MYOGLOBIN.
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Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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PRINTS; PR00613; MYOGLOBIN.
PROSITE; PR01033; GLOBIN; 1.
Heme; Oxygen transport; Transport.
SEQUENCE 154 AA; 17157 WW; 98E
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"Oxygen affithity and amino acid sequence of myoglobins from
endothermic and ectothermic fish.";
Am. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1123-R1133(2001).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73E67F581F79C479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 LHSRHPGDFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO, GO:0005344; Froxygen transporter activity, IEA. GO; GO:0015671; Proxygen transport; IEA. GO; GO:0006810; Prtransport; IEA. InterPro; IPR000371; Globin. InterPro; IPR0003335; Myoglobin.
                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LOSKHPGDFGADAQGAMNKALELFRKDMASNYKELGFQG
                                                                                           DFGADAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AA
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MEDLINE=21146139; PubMed=11247835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan; PF00042; globin; 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
Heme; Oxygen transport; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myoglobin.
Makaira nigricans (Blue marlin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10870 MW;
                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC018001; AAH18001.1;
HSSP; P02185; 111M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                           Similar to myoglobin.
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                          63
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                                                                                                                                                                                                                Q8WVH6
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 EWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DFEMVLKHWGPVEADYATHGNLVLTRLFTEHPETQKLFPKFAGI-AKADMAGNAAISAHG
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"Oxygen affinity and amino acid sequence of myoglobins from endothermic and ectothermic fish.";
Am. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1123-R1133(2001).
EMBL; AF291834; AAG02108.1; ---
GO, GO:0005344; F:oxygen transporter activity; IEA.
GO; GO:0015671; P:oxygen transport; IEA.
GO; GO:0015671; P:oxygen transport; IEA.
InterPro; IPR000931; Globin.
InterPro; IPR000335; Myoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 147;
                                                                                                                                                                                                                                                                                                                                                          40.5%; Score 321.5; DB 13; Length 46.7%; Pred. No. 3.7e-22; rative 20; Mismatches 53; Indels
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SEQUENCE 147 AA, 15797 MW, D0864510EE730506 CRC64;
                                                                                                                                                                                                                                                                                                15842 MW; F52D010973F4D84B CRC64;
HSSP; P02205; 1MYT.
GO; GO:0005344; F:oxygen transporter activity; IEA.
GO; GO:0016571; P:oxygen transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000971; Globin.
InterPro; IPR002335; Myoglobin.
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MEDLINE=21146139; PubMed=11247835;
                                                                                                                                                                                                                                                                 Heme; Oxygen transport; Transport
SEQUENCE 147 AA; 15842 MW; F5
                                                                                                                                                                           Pfam, PF00042; globin, 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00042; globin; 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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InterPro; IPR000971; Globin.
InterPro; IPR002335; Myoglobin.
                                                                                                                                                                                                                                    Pfam, PF00042; globin; 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00042; globin; 1.
PRINTS; PR00613; MYOGLOBIN.
                                                                                                                                                                                                                                                                                                                               Local Similarity 41.2 tes 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    Query Match
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Q9DGI8;
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66 VTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGA 125
                 62 ATVLKKLGELLKAKGSHAAILKPLANSHATKHKIPINNFKLISEVLVKVMHEKAGLDAG- 120
                                                                                                                                                                                                                                                                                                                        TISSUE=Skeletal muscle;
XX MacLines-21146139; Pubbled=11247835;
Amarcinek D.J., Bonaventura J., Wittenberg J.B., Block B.A.;
Marcinek D.J., Bonaventura J., Wittenberg J.B., Block B.A.;
"Oxygen affinity and amino acid sequence of myoglobins from endothermic and ectochermic fish.";
T. Mar. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1123-R1133 (2001).
R. Mar. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1123-R1133 (2001).
R. Mar. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1123-R1133 (2001).
R. Mar. J. Physiol. Proxygen transporter activity; IEA.
GO; GO:0005344; F:oxygen transport; IEA.
R. GO; GO:0006810; P:transport; IEA.
R. InterPro; IPR000971; Globin.
R. InterPro; IPR0009335; Myoglobin.
R. Harr Pro. IPR000335; Myoglobin.
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                                                                                                                                                                                                                   Thumus albacares (Yellowfin tuna) (Neothunnus macropterus).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosfomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Scombroidei,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFam; PF00042; globin; 1.
PRINTS; PR00613; MYCGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
Heme; Oxygen transport; Transport.
SEQUENCE 147 AA; 15660 MW; 3D13814403B48D44 CRC64;
                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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Pred. No. 1.1e-20;
2; Mismatches 58
                                                                                                                                            147 AA
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                                                   126 DAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                   -GQQALRNVMAAVIADLEANYKELGFSG 147
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43.9%; Fr.
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                         Thunnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                     NCBI_TaxID=8236;
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66 VIVLTALGAILKKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGA 125
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Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei; Scombridae; Thunnus.
NCBI_TaxID=8235;
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Katsuwonus pelamis (Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostei,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Scombroidei,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 EWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHG
                                                                                                                                                                                                                             Marcinek D.J., Bonaventura J., Wittenberg J.B., Block B.A.;
"Oxygen affinity and amino acid sequence of myoglobins from endothermic and ectothermic fish.";
Am. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1123-R1133(2001).
EMBL, AF21832; AAG02106.1; -.
HSSP; P02205; 1MYT.
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MEDLINE-21146139; PubMed=11247835;
Marcinek D.J., Bonaventura J., Wittenberg J.B., Block B.A.;
Marcinek D.J., and amino acid sequence of myoglobins from endothermic and ectothermic fish.";
Am. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1123-R1133(2001).
HSSP: P02205; IMYT.
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SEQUENCE 147 AA; 15667 MW; 26114A4B946A1191 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005344; F:oxygen transporter activity; IEA.
GO; GO:0015671; P:oxygen transport; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005344; F:oxygen transporter activity; IEA. GO; GO:0015671; P:oxygen transport; IEA. GO; GO:0016810; P:transport; IEA. InterPro; IPR000971; Globin. InterPro; IPR002335; Myoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.3%; Score 288.5; DB 1
41.2%; Pred. No. 4.4e-19;
iive 25; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA
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                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-21146139; Pubmed=11247835;
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7

147 AA

PRT;

PRELIMINARY;

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Myoglobin.
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          Q7T044
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P79846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRKLGELLKAKGSHAAILKPLANSHATKHKIPINNFRLITEVIGKVMGEK----TGLDAA 115
                                                                                                                                                  70 TALGAILKKKGHHEAELKPLAOSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGADAQG 129
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                                                                                                            64
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                                                                                                     10 VLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHGVTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes; Cottoidei; Hemitripteridae; Hemitripterus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 142;
                                     Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Heart ventricle;
Grove T.J., Sidell B.D.;
"Myoglobin from sea raven, Hemitripterus americanus.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029587; AAK49781.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 AA; 15111 MW; 2DB1EF4602F929D3 CRC64;
           15396 MW; 307DAA2C6D9FDC27 CRC64;
                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005344; F:oxygen transporter activity; IEA.
GO; GO:0015671; P:oxygen transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000971; Globin.
InterPro; IPR002335; Myoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
                                    ; DB 13;
4.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%; Score 285.5; DB 1 44.2%; Pred. No. 7.9e-19;
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                                             43.8%; Pred. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G--AMNKALELFRKDIAAKYKELGYQG 153
                                    36.3%; Score 288; 43.8%; Pred. No. 4
                                                                                                                                                                                                     121 QTALRNVMGIVIADLEANYKELGFTG 146
                                                                                                                                                                                      --AMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                                                   Hemitripterus americanus (Sea raven)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00042; globin; 1.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PS01033; GLOBIN; 1.
Heme; Oxygen transport; Transport.
 Heme; Oxygen transport; Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65, Conservative
                                                              64; Conservative
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        Myoglobin (Fragment).
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             146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  Cottoidei; Hemit:
NCBI_TaxID=8094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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           SEQUENCE
                                     Query Match
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                                                              Matches
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RESULT 9

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66 VIVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Grdell B.D.; Grove T.J., Hendrickson J.W., Sidell B.D.; "Myoglobin Gene Sequence from the Antarctic Notothenioid, Channichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DFDMVLKCWGPVEADHATHGSLVLTRLFTEHPETLKLFPKFAGI-AHGDLAGDAGVSAHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 EWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHG
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Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Notothenioidei; Channichthyidae; Pagetopsis.
                                                                                                                                                                      Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Notothenioidei; Channichthyidae; Channichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Heart ventricle; Vayda M.E., Small D.J., Costello L., Sidell B.D.; Vayda M.E., Yuan M.-L., Small D.J., Costello L., Sidell B.D.; "Extreme conservation of the myoglobin sequence among Antarctic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.7%; Score 283.5; DB 13; Length 147; 42.6%; Pred. No. 1.3e-18; tive 22; Mismatches 56; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY341058; AAQ17544.1; -.
SEQUENCE 147 AA; 15695 MW; 256D05AA3E2DCF76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   notothenioid fishes.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U71152; AAB41673.1;
HSSP; P02205; 1MYT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AA; 14868 MW; 8EDF8F2F32310E80 CRC64;
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GO; GO:0015671; P:oxygen transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000971; Globin.
InterPro; IPR002335; Myoglobin.
PRINTS; PR00613; MYOGLOBIN.
PROSITE; PR00613; GLOBIN; 1.
                                   Last sequence update)
Last annotation update)
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Last annotation update)
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   Created)
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NON TER 1 1 1
SEQUENCE 141 AA; 14868 MW: 8FD
(TrEMBLrel. 25, (TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03,
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                                                                                                                                                       Channichthys rhinoceratus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rhinoceratus.
01-OCT-2003
                                                                               01-OCT-2003
                                           01-OCT-2003
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SEQUENCE FROM N.A.

TISSUB=Heart ventricle;
Vayda M.E., Small D.J., Sidell B.D.;
"Expression of the wyoglobin gene in Antarctic channichthyid fishes.";
(In) Battaglia B., Valencia J., Walton S.W.H. (eds.);
VI SCAR ANTRACTIC COMMUNITIES, pp.1-1, Cambridge University Press,
                                                                                                                                                                                                                                                                                                                                       MEDLINE=98360008; PubMed=9694664;
Small D.J., Vayda M.E., Sidell B.D.;
"A novel vertebrate myoglobin gene containing three A+T-rich introns
is conserved among Antarctic teleost species which differ in myoglobin
                                                 Myoglobin (Fragment).

Notothenia corileeps (black rockcod).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Notothenioidei; Nototheniidae; Notothenia.
         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P02205; IMYT.
GO; GO:0005344; F:oxygen transporter activity; IEA
GO; GO:0015671; P:oxygen transport; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heme; Oxygen transport; Transport.
NON TER 1
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EMBL; U68350; AAC69245.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR000971; Globin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF00042; globin; 1.
PROSITE; PS01033; GLOBIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              TISSUE=Heart ventricle;
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                 60 NKLGDLLKARGAHAALLKPLSSSHATKHKIPIINFKLIAEVIGKVMEEKAGVDAG--GQT 117
                                                                                                                               70 TALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGADAQG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 VTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
                                                                                      10 VLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHGVTVL
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                                          Gaps
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                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
34.2%; Score 271.5; DB 13; Length 141; 42.3%; Pred. No. 1.6e-17; ive 20; Mismatches 59; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Skeletal muscle;
MEDLINE=21146139; PubMed=11247835;
Marcinek D.J., Bonaventura J., Wittenberg J.B., Block B.A.;
"Oxygen affainty and amino acid sequence of myoglobins from endothermic and ectothermic fish.";
Am. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1123-R113
HSSP; P02205; IMYT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS01033, GLOBIN; 1.
Heme; Oxygen transport; Transport.
SEQUENCE 147 AA; 15766 MW; 44EB9A4611EE0366 CRC64;
                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005344; F:oxygen transporter activity; IEA. GO; GO:0015671; P:oxygen transport; IEA. GO; GO:0006810; P:transport; IEA. INCERPO: IPR000371; Globin. InterPro; IPR000335; Myoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 267.5; DB Pred. No. 3.9e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 DAQGAMNKALELFRKDIAAKYKELGYQG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GQTALRNVMGVFIADMDANYKELGFSG 147
                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                        118 GLRNVMAVIIADMEAAYKELGF 139
                                                                                                                                                                                            130 AMNKALELFRKDIAAKYKELGY 151
                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   Scomber japonicus (Chub mackerel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00042; globin; 1.
PRINTS; PR00613; MYOGLOBIN.
                                     60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scombridae; Scomber.
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=13676;
                                                                                                                                                                                                                                                                                                                                                                                    Myoglobin.
      Query Match
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                      Best Local
                                                                                                                                                                                                                                                                                                        Q9DGI9
                                    Matches
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Q98963
ID Q9896
AC Q9896
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69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                             10 VLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHGVTVL
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                              7;
                                                         DB 13; Length 110;
                                                                                                                                                                                                      70 TALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSR 118
                                                                                                                                                                                                                           60 NKLGDLLKARGAHAALLKPLSSSHATKHKIPIINFKLIAEVIGKVMEEK 108
110 AA; 11630 MW; B43B5865F0B6708F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                     29.9%; Score 237.5; DB 13; 45.9%; Pred. No. 1.7e-14; tive 15; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Eye;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                            50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium,
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110 AA

PRT;

PRELIMINARY:

Q98963 Q98963;

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Q8AY74
                                                                                                          RESULT 15
Q8AY74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 KKHGVTVLTALGAILKKKGHHEAE-----LKPLAQSHATKHKIPIKYLEFISEAIIHVLH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LSEGEWOLVLHVWAKVEADVAGHGODILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 LSEAERKAVQATWARLYANCEDVGVAILVRLFVNFPSAKQYFSQFRHMEDPLEMERSPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                             27.1%; Score 215.5; DB 11; Length 190; 31.6%; Pred. No. 3.7e-12; tive 31; Mismatches 68; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.6%; Score 211.5; DB 4; Length 190; Best Local Similarity 31.6%; Pred. No. 8.7e-12; Matches 49; Conservative 30; Mismatches 69; Indels 7
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AX087408; BAC39862.1; -.
MCD; MGI:2144948; Cygb.
GC; GO:0015671; P:oxygen transport; IEA.
InterPro: IPR000937; My0globin.
Pfam; PF00042; globin; 1.
PFam; PR00613; MY0GLOBIN.
PRNINTS; PR00613; MY0GLOBIN.
PROSITE; PS01033; GLOBIN; 1.
SEQUENCE 190 AA; 21431 MW; 867AS04D521CC09F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIGHT, PROCEST, MYCGLOBIN.
PROSITE; PRO1033, GLOBIN; 1.
Hypothetical protein; Heme; Oxygen transport; Transport.
SEQUENCE 190 AA; 21377 MM; 1BD536484CC6AL04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BCC2798, AA129798.1; -...
GO; GO:0005737; C:cytoplasm; ISS.
GO; GO:0005374; F:cytoplasm; ISS.
GO; GO:0005374; F:cytoplasm; ISS.
GO; GO:0004601; F:peroxidase activity; ISS.
GO; GO:0015671; P:cxygen transport; NAS.
GO; GO:0006979; P:response to oxidative stress; ISS.
InterPro; IPR002335; Myoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Home sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 EEFANDFPVETQKAWAXLRGLIYSHVTAAYKEVGW 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 SRHPGDFGADAQGAMNKALELFRKDIAAKYKELGY 151
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 31.6*
Matches 49; Conservative
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TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
OGNEXS
AC OGNEXX
AC OGNEXX
AC OGNEXX
DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC DT 01-OC D
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61

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65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grove T.J., Hendrickson J.W., Sidell B.D.;
Grove T.J., Hendrickson J.W., Sidell B.D.;
"Myoglobin gene sequence from Champsocephalus esox, a notothenioid
"Myoglobin gene sequence from Champsocephalus esox, a notothenioid
"Ish that lacks myoglobin expression.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AFS47166, AAM52371.1;
-
EMBL, AFS47166, AAM52371.1;
-
InterPro; IPR000971; Globin.
InterPro; IPR000971; Globin.
InterPro; IPR00042; Globin;
InterPro; PR00042; Globin;
PRINTS; PR00042; GLOBIN;
PROSITE; PS01033; GLOBIN;
PROSITE; PS01033; GLOBIN;
                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Notothenioidei; Channichthyidae; Champsocephalus.
NCBI_TaxID=159716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٦;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.5%; Score 194.5; DB 13; Length 103; 44.4%; Pred. No. 1.6e-10; ive 14; Mismatches 35; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 AA; 10723 MW; 13ACD2D54A1F99E8 CRC64;
                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
137 EEFASDFPPETQRAWAKLRGLIYSHVTAAYKEVGW 171
                                                                                                                                                                                    Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 VTVLTALGAILKKKGHHEAELKPLAQSHAT 95
                                                                                                                                                                                    103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ATVLNKLGDLLKARGAHAALPKPLSSSHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 10, 2004, 15:28:40 Job time : 19.3378 secs
                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 44.4%
Matches 40; Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                   Champsocephalus esox.
                                                                                                                                                                                                                                                                                                                                       Truncated myoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

August 10, 2004, 15:18:30 ; Search time 31.8547 Seconds (without alignments) 1632.058 Million cell updates/sec Run on:

US-09-455-978B-77

1 MSNDNDTLVTADVRNGIDGH...........DELVARFLPMLKLLTFDQQI 184 score: Sequence: Title: Perfect :

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2001s:* geneseqp2000s:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aae04641 Halohacte		Bacil		0 Protein	3 Protein	4 Streptoc				œ				LC.		Leis		Abu37440 Protein e	6	Por	_		7 Human	9 Acinet
SUMMARIES	T)	AAE04641	AAE04677	AAE04642	AAP70493	AAP95030	AAR07013	AAR10004	AAR53290	AAY34570	AAY34569	AAY34568	AAY34428	AAR07014	AAR62944	AAR10005	AAR57365	AAW03691	ABU38101	ABU37440	ABP79309	AAY34454	AAY34330	AAB07677	ADC31377	ADA33559
	DB	4	4	4	М	Н	7	7	7	7	7	~	7	N	N	~	~	7	9	9	9	7	7	m	7	9
	Length	489	39	432	448	448	448	448	448	1175	1232	1266	1269	593	593	594	955	955	202	496	505	523	533	318	483	302
de	Query Match	100.0	21.8	15.2	10.6	10.6	10.6	10.6		10.6		10.6	10.6	10.5			9.5	٠	9.4		9.3	9.3	•	•	9.5	9.5
	Score	933	203	142	66	66	66	66	66	66	66	66	66	98	98	86	83	89	88	83	87	87	87	86.5	86	85.5
	Result No.	п	73	m	4	Ω	9	7	8		10	11	12	13	14	15		17	18	19	20	21	22	23		25

Aay75098 Neisseria	Abu38184 Protein e	Abu32037 Protein e	Abb91977 Herbicida	Abu25854 Protein e	Abu02251 S. pneumo	Abb62080 Drosophil	Abu34054 Protein e	Abu41908 Protein e	Aaq91714 C glutami				Add24123 Bacteriop	Abq94315 RNA phage		Abu37640 Protein e			
AAY75098	ABU38184	ABU32037	ABB91977	ABU25854	ABU02251	ABB62080	ABU34054	ABU41908	AAG91714	ABU33824	ABR56445	ABR44548	ADD24123	ABG94315	ABU27622	ABU37640	AAB41460	ABP04390	ABJ26182
3	9	9	Ŋ	9	9	4	9	9	4	9	9	9	7	Ŋ	9	G	m	w	9
2599	2703	315	712	1254	4384	319	403	695	831	928	329	329	329	330	1333	2799	248	248	1178
9.1	9.1	8.9	8.9	8.9	8.9	8 6.	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.7	8.7	8.7
85	82	83.5	83.5	83.5	83.5	83	82.5	82.5	82.5	82.5	82	82	82	82	82	82	81	81	81
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Halobacterium salinarium HemAT-Hs protein. AAE04641 standard; protein; 489 AA. (first entry) (revised) 11-SEP-2003 04-SEP-2001 AAE04641; RESULT 1

Haem binding protein; HemAT-Hs; HemAT-B8; gaseous ligand sensor; oxygen storage; artificial photosynthesis; signalling function; alpha-haemoglobin; myoglobin; therapy.

Halobacterium salinarum.

WO200140475-A2.

07-JUN-2001.

05-DEC-2000; 2000WO-US033048.

99US-00455978. 06-DEC-1999;

(UYHA-) UNIV HAWAII.

Alam M, Larsen R;

WPI; 2001-374832/39.

N-PSDB; AAD08991

Novel isolated bacterial heme binding protein, HemAT-Hs or HemAT-Bs which reversibly binds oxygen with low affinity, useful for controlled storage of oxygen and for sensing gaseous ligands such as oxygen.

Claim 6; Page 10; 94pp; English.

binding protein, HemAT-Hs or HemAT-Bs which reversibly binds oxygen with low affinity. Haem binding protein is useful for controlled storage of oxygen by allowing haem binding protein to bind and store oxygen, and triggering the release of oxygen from haem binding protein by activating the signalling domain. Haem binding protein is useful for sensing gaseous ligands such as oxygen, NO, CO, or CN. Blood substitute comprising haem binding protein is useful for treating a patient suffering from low blood levels by administering and regulating the oxygen binding of the haembinding protein by modifying the signalling domain. Haem binding protein The present invention relates to isolated archeal and bacterial haem

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                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to isolated archeal and bacterial haem binding protein, HemAT-Hs or HemAT-Bs which reversibly binds oxygen with low affinity. Haem binding protein is useful for controlled storage of
                                                                                                                                                                                                                          ADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG 120
                                                                                                                                                                                                                                                     61 ADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG 120
                                                                                                                                                                                                                                                                                KIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTF 180
                                                                                                                                                                                              9
                                                                                                                                                                     09
          identifying potential signalling functions of mutated alpha-haemoglobin and myoglobin causing several diseases. The present sequence is Halobacterium salinarium HemAT-HS protein which is salt tolerant. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                useful for haem-based catalysis, for artificial photosynthesis and
                                                                                                                                                                    1 MSNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEAT
                                                                                                                                                                                                1 MSNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEAT
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haem protein related Halobacterium salinarium protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I-Hs; HemAT-Bs; gaseous ligand sensor photosynthesis; signalling function;
                                                                                                                                         .
0
                                                                                                             Length 489;
                                                                                                                                        Indels
                                                                                                                                         0
                                                                                                             Score 933; DB 4;
Pred. No. 2.6e-89;
                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haem binding protein, HemAT-Hs, HemAT.
oxygen storage, artificial photosynthe
alpha-haemoglobin, myoglobin, therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
19. .39
/label= M2_Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 16; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE04677 standard; peptide; 39 AA
                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00455978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2000; 2000WO-US033048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                         184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium salinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-374832/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UYHA-) UNIV HAWAII
                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larsen R;
                                                                                                                                                                                                                                                                                                                                         DQQI 184
                                                                                                                                                                                                                                                                                                                                                                     DÓQI 184
                                                                                  Sequence 489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200140475-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE04677;
                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                         181
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
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The present invention relates to isolated archeal and bacterial haem binding protein, HemAT-Hs or HemAT-Bs which reversibly binds oxygen with low affinity. Haem binding protein is useful for controlled storage of oxygen by allowing haem binding protein is useful for sore oxygen, and triggering the release of oxygen from haem binding protein by activating the signalling domain. Haem binding protein is useful for sensing gaseous binding protein is useful for treating a patient suffering from low blood levels by administering and regulating the oxygen binding of the haem-binding protein by modifying the signalling domain. Haem binding protein is useful for tareating signalling domain. Haem binding protein is useful for haem-based catalysis, for artificial photosynthesis and for identifying potential signalling functions of mutated alpha-haemoglobin
                                                                                                                                                                                                                                                                                                                                                           0;
oxygen by allowing haem binding protein to bind and store oxygen, and triggering the release of oxygen from haem binding protein by activating the signalling domain. Heem binding protein is useful for sensing gaseous binding such as oxygen, No. CO, or CN. Blood substitute comprising haem binding protein is useful for treating a patient suffering from low blood levels by administering and regulating the oxygen binding of the haembinding protein by modifying the signalling domain. Heem binding protein is useful for heem-based catalysis, for artificial photosynthesis and for identifying potential signalling functions of mutated alpha-haemoglobin and myoglobin causing several diseases. The present sequence is a haem protein related Halobacterium salinarium protein fragment. (Updated on II-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated bacterial heme binding protein, HemAT-Hs or HemAT-Bs which reversibly binds oxygen with low affinity, useful for controlled storage of oxygen and for sensing gaseous ligands such as oxygen.
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haem binding protein; HemAT-Hs; HemAT-Bs; gaseous ligand sensor; oxygen storage; artificial photosynthesis; signalling function; alpha-haemoglobin; myoglobin; therapy.
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                                                                                                                                                                                                                                                                                                                 Score 203; DB 4; Length 39;
Pred. No. 6e-14;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   134
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                                                                                                                                                                                                                                                                                                                                                                                                                           QAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYL
                                                                                                                                                                                                                                                                                                                                                                                                   96 QAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis HemAT-Bs protein.
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                                                                                                                                                                                                                                                                                                    21.8%; Scc.
100.0%; Pre
0; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE04642 standard, protein; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-2000; 2000WO-US033048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00455978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYHA-) UNIV HAWAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-374832/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larsen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD08992
                                                                                                                                                                                                                                                                               Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200140475-A2.
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                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE04642
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20-JUN-1988;
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                                                                                                                                                                                                                                                                                                                                Protein G
                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                     AAP95030;
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                                                                                                               QLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALAD 150
                                                                                                                         31 AEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVE 90
                                                                                                90
and myoglobin causing several diseases. The present sequence is Bacillus
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloned Protein G gene - used for producing Protein G for detection purificn. of antibodies and treatment of diseases.
                                                              10;
                                           4.8e-06;
ches 76; Indels
                                                                                                                                                 151 DVVADRGEEAAAVDELVARFLPMLKLLTFDQQI 184
                                                                                                                                                                 -----EASITNQOELLKAIKATTKILNLEQQL 175
                                                                                                                                                                                                                                                                                                                     G strain'.
                                           ; Score 142; DB
; Pred. No. 4.8e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                               228. .297
/label= active site
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/label= active site
                                                                                                                                                                                                                                                                                                                   sp; 'Lancefield Group
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                  Protein G; antibody; Fc receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 68pp; English
                                                                                                                                                                                                             AAP70493 standard; protein; 448
                                          15.2%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                           87WO-US000329
                                                                                                                                                                                                                                                                                                                                                                                                                                           86US-00829354
86US-00854887
                                     Query Match
Best Local Similarity 25.35
Matches 39; Conservative
                                                                                                                                                                                                                                                                 (first entry)
        subtilis HemAT-Bs protein
                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEMX ) GENEX CORP. (FAHN/) FAHNESTOCK S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1987-250197/35.
                          Sequence 432 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahnestock SR;
                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                              27-AUG-2003
25-MAR-2003
06-MAR-1991
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23-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                       WO8705025-A.
                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1987
                                                                                                                                                                                                                                                                                                                                              Active-site
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                                                                                                                                                                                                                                                                                 Protein G.
                                                                                                                                                                                                                              AAP70493;
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8
non-pathogenic host. Suitable cloning vectors are lambda gtll, Ml3mp9 and ggZ1066. (Updated on 25-MR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                         54 ----QPLFEATADAL-----VTDFYDHLESYERIQDLFANSTKTVEQLKETQAEYLLG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GLSDFLKSQTPA---EDTVK 175
                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                                                                                                                                                              97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein G of non-pathogenic streptococcus and variants may be isolated, useful as bacterial Fc receptors eg in purification and detection of Abs. screening of hybridoma clones and treatment of disease. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                          72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloned protein G variant genes - expressing proteins having immunoglobulin-binding properties of protein G and derived from
                                                                                                                                                                                                                                                                                           ---DIMAALAAE-
                                                                                                                                                                                    10.6%; Score 99; DB 1; Length 448; 25.3%; Pred. No. 0.17; ive 25; Mismatches 45; Indels
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                      10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein G; immunoglobulin; Fc receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ESAKKARİSEATD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP95030 standard; protein; 448 AA.
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                                                                                                                                                       Query Match
Best Local Similarity 25.3%
Rest Local Similarity 25.3%
A8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 AVDELVARFL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 SIELAEAKVĽ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEMX ) GENEX CORP.
(PHAA ) PHARMACIA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1989-023848/03.
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                                                                                                                                 Sequence 448 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
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Length 448;

DB 1;

Score 99;

10.6%;

8

Gaps

72;

45;

Length 448; Indels 97

----GLSDFLKSQTPA---EDTVK 175

us-09-455-978b-77.rag

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Protein G gene product may be modified allowing the variant to be imobilised and exhibit different binding profiles. The bound protein is useful in purification and detection of 1gs and fragments. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                  54 ----QPLFEATADAL-----VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
                                                                                                                                                103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
                                                                                                                  41 TPIIRNGGE---LINLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAAAWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immobilised protein G variants - used for detection, isolation and purificn. immunoglobulin(s) and immunoglobulin fragments.
                                                       10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD---
        10.6%; Score 99; DB 2; 25.3%; Pred. No. 0.17; iive 25; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                 228. .282
/label= Active site Bl
298. .352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298. .352
/label= Active site B2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 8; 52pp; English.
                                                                                                                                                                                                                                                                                AAR10004 standard; protein; 448
                                                                                                                                                                   : |||::||
------ESAKKARISEATD
                                                                                                                                                                                                                                                                                                                                                                          Ö
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86US-00854887.
87WO-US000329.
87US-00063959.
88US-00209236.
                                                                                                                                                                                                                                                                                                                                                                          Streptococcus GX7809 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-00354264
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                  48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus sp; GX7809
                                                                                                                                                                                                 163 AVDELVARFL 172
                                                                                                                                                                                                                176 SIELAEAKVL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee T,
                                                                                                                                                                                                                                                                                                                             (revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulins; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-006758/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMX ) GENEX CORP
          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ10001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fahnestock SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1986;
17-FEB-1987;
19-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAY-1989;
                                                                                                                                                                                                                                                                                                                             24-OCT-2003
25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                    13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Active-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-1988
                                                                                                                                                                                                                                                                                                       AAR10004;
                                                                                                                                                                          146
                                  Matches
                                                                                                                                                                                                                                                                    AAR10004
                                                                                                                                                                                                                                                         RESULT
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             8
                                                                                 54 ----QPLFEATADAL-----VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
                                                                                                103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEBAAA 162
                                                                                                                                                    ----GLSDFLKSQTPA---EDTVK 175
                                                          97
                                                    41 TPIIRNGGE---LTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAABA
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding immunoglobulin.
             72;
                                    10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD-----DTMAALAAE---
             Indels
             45;
 Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus sp; Lancefield Group G strain.
             25; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Protein G variant with two active sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 8a-c; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                           Ą.
                                                                                                                                                    -----ESAKKARISEATD-
                                                                                                                                                                                                                                                           AAR07013 standard; protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86US-00829354.
86US-00854887.
87WO-US000329.
87US-00063959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88US-00209236
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      228. .282
/label= B1
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/label= B2
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               48; Conservative
                                                                                                                                                                           AVDELVARFL 172
                                                                                                                                                                                           SIELAEAKVL 185
                                                                                                                                                                                                                                                                                                          (revised)
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N-PSDB; AAQ06018.
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   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 448 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMX ) GENEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1986;
17-FEB-1987;
19-JUN-1987;
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25-MAR-2003
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                                                                                                                                                      146
                                                                                                                                                                            163
                                                                                                                                                                                                  176
               Matches
                                                                                                                                                                                                                                    RESULT 6
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8

Gaps

72;

97

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54 ----QPLFEATADAL-----VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
                                                                                                                                                                                                                              103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
           A 1.9kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7809. The Protein G has IgG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domains are claimed. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                   -----GLSDFLKSQTPA---EDTVK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas gingivalis, PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                           ----INNAKTVEGIKDLOAQVV--
                                                                                                                                                 --DIMAALAAE-
                                                                                                       DB 2; Length 448; 0.17;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rothel LJ,
                                                                                                                            45;
                                                                                                                                               10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patterson MA, Agius CT,
                                                                                                      10.6%; Score 99; DB 25.3%; Pred. No. 0.17:ive 25; Mismatches
                                                                                                                                                                                                    Porphorymonas gingivalis protein PG9.
                                                                                                                                                                                                                                                                                                                                           AAY34570 standard; protein; 1175 AA.
                                                                                                                                                                                                                                                  -----ESAKKARISEATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98AU-00001546.
98AU-00002264.
98AU-00002911.
98AU-00003128.
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98AU-00003654.
98AU-00004917.
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98AU-00005028
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                Local Similarity 25.3
les 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                       163 AVDELVARFL 172
                                                                                                                                                                                                                                                                                        176 SIELAEAKVL 185
                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rr IG, Pa
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-385613/32.
N-PSDB; AAX91788.
                                                                                   Sequence 448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CSTC-) CST TLD
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10-MAR-1998;
09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1998;
29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hocking DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998;
05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigenic.
                                                                                                                                                                                                                                                                                                                                                                AAY34570;
                                                                                                                                                                                                                                                   146
                                                                                                       Query Match
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                                                                                                                  Best Loca
Matches
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                                                                                                           ----QPLFEATADAL------VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
                                                                                                                         LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
                                                                                                                                                                        ----GLSDFLKSQTPA---EDTVK 175
                                                                        53
                                                                                        TPIIRNGGE---LINLLGNSETTLALRNEESATADLTAAAVADTVAAAAAEA 97
                                                                                                                                                                                                                                                                                                                                                                      Protein G; variant; IgG binding activity; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant streptococcal protein G variants - useful for antibody
                                                    Gaps
                                                   72;
                                                                    10 TADVRNGIDGHALADRIGLDEABIAWRLSFTGIDD-----DTMAALAAB---
                                Length 448;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                  Streptococcus Protein G derived from strain GX7809
                                                   45;
                             DB 2;
0.17;
                      detection and purification and for therapy.
                                                                                                                                                                                                                                                                                                                                                                               Lancefield Group G; bacterial Fc receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 3 and Fig 8; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  228. .282
| Jabel= B1
283. .297
| Jabel= b
| Yote= "linking region"
298. .352
| Jabel= B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PHAA ) PHARMACIA LKB BIOTECHNOLOGY AB
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                 AAR53290 standard; protein; 448 AA
                                                                                                                                                                 86US-00854887.
87US-00063959.
88US-00209236.
90US-00540169.
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                                                                                                                                                                                                                                                                                                                              (first entry)
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     sp. GX7805.
                                                                                                                                                                                           AVDELVARFL 172
                                                                                                                                                                                                               SIELAEAKVL 185
                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-159179/19.
                                       Local Similarity
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         Sequence 448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
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19-JUN-1987;
20-JUN-1988;
19-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1992;
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06-JAN-1995
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Active-site
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                                                 48;
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                                                                                                                                                                                                                                                                                     AAR53290;
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                                                                                                                                                                                                               176
                           Query Match
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                                                  Matches
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Margetts MB;

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504 HSSGKTTFLSQYDINYTYQ-----KNTHVLSIHRSNNPNAIFYDFGGQDYYHGIYQAFFT 558
                                                                                                                                                               Porphorymonas gingivals (PC) polypeptide sequences given in AAY4318 to AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivals. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 RIHDNPFVASSGLILSPYDNHL-----PEIKALLEKEKEKÇKKTSVEYHPFCKVMLLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GPDVYLGAYTRYYT
                                                                                  Antigenic Porphorymonas gingivalis peptides for preventing gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 GLDGLÁSLTRLSLRRNQISKLEGLDRLKVLRKLDVSGNDIQSIDDIKLLAPILEÓTLEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GIDGHALADRI-----GLDEAEIAWRLSFTG----IDDDTMAALAAEQPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEY----LLG-
                                                                                                                                                     AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                               Length 1232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LGR----GEYDTEYAAQRARIGKIHDVLGL-----
                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 99; DB 2; 25.6%; Pred. No. 0.71; iive 23; Mismatches 4
                                                                                                                     Claim 1; Page 563-565; 588pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas gingivalis protein PG9
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98AU-00003338.
98AU-00003654.
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98AU-00001546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                WPI; 1999-385613/32.
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                Sequence 1232 AA;
                                                 N-PSDB; AAX91787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1998;
22-MAY-1998;
29-JUL-1998;
30-JUL-1998;
04-AUG-1998;
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09-APR-1998
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20-MAR-2003
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Hocking DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 RIHDNPFVASSGLILSPYDNHL-----PEIKALLEKEKEKOKKTSVEYHPFCKVMLLGN 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LGR----GEYDTEYAAQRARIGKIHDVLGL-------GPDVYLGAYTRYYT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501
                                                                                PAX91536 to PAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY34363. AAX91802 to AAX91898 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                      ----GLDEAEIAWRLSFTG-----IDDDTMAALAAEQPL--- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Margetts MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 HSSGKTTFLSQYDTNYTYQ-----KNTHVLSIHRSNNPNAIFYDFGGQDYYHGIYQAFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEY-----LLLG-
                  Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                   DB 2; Length 1175;
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                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                 10.6%; Score 99; DB 2; 25.6%; Pred. No. 0.66; ive 23; Mismatches
                                                      Claim 1; Page 565-567; 588pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY34569 standard; protein; 1232 AA
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98AU-00003128.
98AU-00003338.
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98AU-00001546
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                                                                                                                                                                                                                                                                                                                                                      46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        16 GIDGHALADRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(revised)
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                  Sequence 1175 AA;
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10-MAR-1998;
09-APR-1998;
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29-JUL-1998;
30-JUL-1998;
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05-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
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29-JUL-1998;
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Matches
                                                                                                                                            Ross
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                                                                                                                                                                                                                                          AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX94318 to AAX943683. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease (Updated on 27-AUG-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                            Rothel LJ, Margetts MB;
                                                                                                                                                                    Antigenic Porphorymonas gingivalis peptides for preventing gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 GLDGLASLTRLSLRRNQISKLEGLDRLKVLRKLDVSGNDIQSIDDIKLLAPILEQTLEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 RIHDNPFVASSGLILSPYDNHL-----PEIKALLEKEKEKQKKTSVEYHPFCKVMLLGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 99; DB 2; Length 1266;
; Pred. No. 0.74;
23; Mismatches 47; Indels
                                                          Agius CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LGR----GEYDTEYAAQRARIGKIHDVLGL-
                                                                                                                                                                                                       Claim 1; Page 560-563; 588pp; English.
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                                                        Patterson MA,
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98AU-00001546.
98AU-00002264.
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25.6%;
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                                                                            Webb EA;
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                                                                                                             WPI; 1999-385613/32
                                                      Barr IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1266 AA;
                                                                                                                                N-PSDB; AAX91786
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23-APR-1998;
05-MAY-1998;
                                                                          Hocking DM,
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25-AUG-1999
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10-MAR-1998
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                                                    BC,
                                                      Ross
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AAY34428
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                                                                                                                                                     Margetts MB;
                                                                                                                                                                                                                                                                      Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 ----FEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEX-----LLG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 99; DB 2; Length 1269; 
; Pred. No. 0.74; 
23; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Indels
                                                                                                                                                 Rothel LJ,
                                                                                                                                               Agius CT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 --LGR----GEYDTEYAAQRARIGKIHDVLGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein G variant with three active sites
                                                                                                                                                                                                                                                                                                                Claim 1; Page 401-403; 588pp; English.
                                                                                                                                                 Patterson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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               98AU-00004917.
98AU-00004963.
98AU-00005028.
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98AU-00003654
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/label= B1
373. .427
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443. .497
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hes 46; Conservative
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                                                                                                                                             Barr IG, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                          WPI; 1999-385613/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1269 AA;
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                                                                                                   (CSTC-) CST TID
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                                                         04-AUG-1998;
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25-MAR-2003
17-JAN-1991
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92US-00871539
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/label= C2
541. .545
/label= C3
546. .550
/label= C4
511. .555
/label= C5
                                                   label= A3
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                                                                                                               label= b
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                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 593 AA;
                                                           Misc-difference
                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fahnestock SR;
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19-JUN-1987;
20-JUN-1988;
19-JUN-1990;
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                                                                                                                                                                                  Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed at high levels. The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                               103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
                                                                                                                                                                                                                                                                                                                                                                                        -------GLSDFLKSQTPA---EDTVK 175
                                                                                                                                                                                                                                                                                                                                      54 ----QPLFEATADAL-----VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor.
                                                                                                                                                                                                                                                                                                              10 TADVRNGIDGHALADRIGLDEAELAWRLSFTGIDD-----DIMAALAAE-----
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                          Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding immunoglobulin.
                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                10.5%; Score 98; DB 2; Length 593; 25.3%; Pred. No. 0.32; ive 25; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus Protein G derived from strain GX7805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
106. .140
/label= A1
141. .178
/label= a1
/note= "linking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR62944 standard; protein; 593 AA.
                                                                                                                                                                    Disclosure; Fig 9; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                           ------ESAKKARISEATD
                                             86US-00854887.
87WO-US000329.
87US-00063959.
                  88US-00209236
                                    86US-00829354
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.3%
Matches 48, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus sp. GX7805.
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                                                                                                                                                                                                                                                                                                                                                                                                            163 AVDELVARFL 172
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                                                                                                                  WPI; 1990-297491/39.
N-PSDB; AAQ06019.
                                                                                CORP.
                                                                                                                                                                                                                                                  Sequence 593 AA;
                                                                               (GEMX ) GENEX
                                                                                                 Fahnestock SR
                                              23-APR-1986;
17-FEB-1987;
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10-JAN-1995
                   20-JUN-1988;
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                                    14-FEB-1986;
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Active-site 30. .354

Misc-difference 200-si .370

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Active-site 30. .372

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Active-site 30. .372

Misc-difference 30. .372

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                                                                                     54 ----QPLFEATADAL-----VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
                                                                                                            ----INNAKTVEGVKDLQAQVV-- 145
                                                                                                                               103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
                                                                                                                                                     ----GLSDFLKSQTPA---EDTVK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein G gene product may be modified allowing the variant to be
imobilised and exhibit different binding profiles. The bound protein is
useful in purification and detection of Igs and fragments. (Updated on 25
                                                53
                                                                    97
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immobilised protein G variants - used for detection, isolation and purificn. immunoglobulin(s) and immunoglobulin fragments.
                         72;
                                             --DTMAALAAE--
ch 10.5%; Score 98; DB 2; Length 593; I Similarity 25.3%; Pred. No. 0.32; 48; Conservative 25; Mismatches 45; Indels
                                          10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD-
                                                                                                     98 AAAADALAKAKADALKEFNKYGVSDYYKNL----
                                                                                                                                                                                                                                                                                                                                                                                                                         304. .358
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444. .498
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                                                                                                                                                                                                                                                      AAR10005 standard; protein; 594 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 9; 52pp; English.
                                                                                                                                                      -----ESAKKARISEATD-
                                                                                                                                                                                                                                                                                                                                            Streptococcus GX7805 protein G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86US-00829354.
86US-00854887.
87WO-US000329.
87US-00063959.
88US-00209236.
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                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus sp; GX7805.
                                                                                                                                                                                         SIELAEAKVL 185
                                                                                                                                                                           163 AVDELVARFL 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fahnestock SR, Lee T,
                                                                                                                                                                                                                                                                                                                                                                Immunoglobulins; Ig.
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N-PSDB; AAQ10002.
Query Match
Best Local Similarity
Matches 48; Conserv
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23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
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25-MAR-2003
13-MAR-1991
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                                                                                                                                                                                                                                                                                                                                     -----GLSDFLKSQTPA---EDTVK 175
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                                                                                                                                                              --DTMAALAAE-----
                                                                                                                             Gaps
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                                                                                   Query Match
10.5%; Score 98; DB 2; Length 594;
Best Local Similarity 25.3%; Pred. No. 0.32;
Matches 48; Conservative 25; Mismatches 45; Indels
                                                                                                                                                       10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD----
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Job time : 33.8547 secs
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1 MSNDNDTLVTADVRNGIDGH......DELVARFLPMLKLLTFDQQI 184
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:* Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	;		equence 2,	equence 1	Segmence 1, App	Semienci	36 Semienci	19 Sequence	4 Sequence	Segment 0	Segment	Sequence	Semience	Segment	Sedimens	Semience C economics	o de la la	Segmence 3. Appli	Seguence 3. App	equence	egnence	Semience 6943 A	Semience 11103	Part Somether	equence 2100	Semience	Semience 34
SUMMARIES	ID	- 4	-08-		894-00324-	(*)	-489-039A-88	-252-991A-	US-09-252-991A-3001	-252-991A-1	-252-991A-32	-252-991A-18	-540-236-259	936-2	352-5		PCT-US93-07923-2	491A-	08-619-280A-	-08-940-39	09-794	10-002-59	-328-35	09-489-039A-	-09-252-991A-1	52-991A-2	-09-252-991A-1	-08-976-063E-34
	Length DB	955 2				·	319 4	542 4	1253 4	700 4	553 4	677 4	438 4	878 3	733 4	755 5	759 5	766 1	766 1	766 2	766 4	766 4	443 4	510 4	297 4	320 4	579 4	531 4
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77; Indels

70 DHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTE-YAAQRARIGKIHDVLGL 128

13 VRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVT---DFY 69

9.8%; Score 91.5; DB 2; Length 955; 27.3%; Pred. No. 0.16; tive 22; Mismatches 77; Indels 4E

Query Match
Best Local Similarity 27.33
Matches 54; Conservative

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Segmence 19796.	Segmence 4946. An																N	
US-09-252-991A-19796	US-09-134-000C-4946	US-09-134-001C-3390	US-09-489-039A-8350	US-09-540-236-2074	US-09-107-532A-7201	US-09-107-532A-6248	US-09-252-991A-19611	US-09-252-991A-33114	US-09-252-991A-19607	US-08-669-408B-10	PCT-US93-03076-4	US-09-134-001C-4522	US-08-714-741-32	US-09-252-991A-30957	US-09-252-991A-29072	US-09-394-200-2	US-10-047-757-2	
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620	522	634	490	892	550	717	169	250	250	413	778	1186	8991	571	700	983	983	
8.1	8.1	8.1	8.0	8.0	8.0	8.0	8.0	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.8	7.8	7.8	
16	75.5	75.5	75	75	74.5	74.5	74.5	74	73.5	73.5	73.5	73.5	73.5	73	73	73	73	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

389414

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Sequence 3, Application US/08428414A
Patent No. 5912166
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVENTION: LEISHMANIASIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: EN PC compatible
COMPUTER: BM PC compatible
COMPUTER: Ploppy disk
COMPUTER: PLEM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,414A
FILING DATE: 21-APR-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Kadlecek, Ann T.
REGISTRATION NUMBER: 39,244
REFERBENCE/DOCKET NUMBER: 210121.407
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: TELEFAX (206) 682-400 TELEFAX 37265 682-6031 TELEX: 3723836 SEBANDERRY INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: : 955 amino acids amino acid CITY: Seattle STATE: Washington COUNTRY: USA linear ZIP: 98104-7092 STRANDEDNESS ; TOPOLOGY: US-08-428-414A-3 US-08-428-414A-3 LENGTH:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602 TOLSOVVTDRERLTRDLORIOYEYGETELARDVALCAAOEMEARYHAAVFHLOTLLELAT 661
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                                                                       69; Indels 30; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 LGLGRGEYDTE-YAAQRARIGKIHDVLGLGPDVYLGA----YTRYYTGLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 955;
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Jeffrey B. Oster
STREET: 8339 SE 57th Street
CITY: Mercer Island
STATE: Machington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 89; DB 1 ilarity 29.3%; Pred. No. 0.3; Conservative 19; Mismatches
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ZIP: 98040-4906
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTARE: WORD for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676B
FILING DATE: 15-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: OSter, Jeffrey B.
REGISTRATION NUMBER: 32,585
REFRENCE/DOCKET NUMBER: REED-4
TELEPHONE: (206) 232 7845
TELEPHONE: (206) 236 0205
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                 Sequence 1, Application US/08006676B Patent No. 5411865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/08282845; Patent No. 5719263; GENERAL INFORMATION:
                                                      129 GPDVYLGA----YTRYYTGLL---
                                                                                                                            169 -- ARFLPMLKLLTFDQQI 184
                                                                                                                                                            691 ONARESACERLTSLEÇÇL 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-006-676B-1
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US-08-282-845-2
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44 DDTMAALAAEQPLFEATADALVT---DFYDHLESYERTQDLFANSTKTVEQLKETQAEYL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 ESTVAQLEREQREREVALDALQTHQRKLQEALESSERTA---AERDQLLQQLTELQSB-R 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602 TQLSQVVTDRERLTRDLQRİQYEYGETELARDVALCAAQEMEARYHAAVFHLQTLLELAT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 ---DALADDVVADRGEEAAAAVDELV----ARFLPMLKLLTFDQQI 184
TITLE OF INVENTION: A 230Kd Antigen Present in Leishmania
TITLE OF INVENTION: Species
TUMBER OF SEQUENCES: 3
CORRESPONDENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
9.5%; Score 89; DB 1; Length 955;
Best Local Similarity 29.3%; Pred. No. 0.3;
Matches 49; Conservative 19; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Apple Macintosh Operating System 7.1 SOFTWARE: Microsoft Word for Macintosh 5.1a CURRENT APPLICATION DATA: BAPPLICATION NUMBER: US/08/282,845
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GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/006,676
FILING DATE: JANUARY 15, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORWATION:
NAME: Perking, Parricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5004-A
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STREET: 51 University Street
CITY: Seattle
STATE: Washington
                                                                                                                                                                       ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 955 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-282-845-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         Seattle
                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                    COUNTRY:
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COMPUTER: Apple Macintosh

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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21396
                                                                                                                                                                                             APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9%; Score 83.5; DB 4; Length 319; 25.4%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 82; DB 4; Length 542;
25.3%; Pred. No. 0.84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 RNGIDGHALADRIGLDEAEIA-WRLSFTGIDDDTMAALAAEQPLF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
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                                                                                                                                                                                                                                                          FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A.
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21396, Application US/09252991A Patent No. 6551795
                                                                                                                             Sequence 8872, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 ADDVVADRGEEAAAAVDELVA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 VDPGYAESGRRAARQLIEQIA 304
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
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            289 PNVRLG 294
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                                                                              RESULT 6
US-09-489-039A-8872
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APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 DDTMAALAAEQPLFEATADALVT---DFYDHLESYERTQDLFANSTKTVEQLKETQAEYL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 RIGL---DEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    662 EWEDALRERALAERDEAAAAELDAAASTSQNARESACERLTSLEQQL 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 85.5; DB 4; Length 302;
; Pred. No. 0.14;
23; Mismatches 41; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
9.5%; Score 89; DB EBest Local Similarity 29.3%; Pred. No. 0.3; Matches 49; Conservative 19; Mismatches
                           Word, version 5.1a
                                                                                                                   CLASSIFLALIUM:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676
FILING DATE: 15-JAN-1993
ATTORNEY AGENT INFORMATION:
NAME: PETKINS, PATRICIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-WO
TELECOMUNICATION INFORMATION:
TELECHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENEMAN. GARACTERISTICS:
                   SOFTWARE: Microsoft Word, version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00324
Apple System 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4846, Application US/09328352; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.2%;
Best Local Similarity 29.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / MOLECULE TYPE: protein
PCT-US94-00324-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                     FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-328-352-4846
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LENGTH: 302
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à a ð g ò ----DNDTLAALVAN--LVEADLL 180

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----VADRGEE-

47;

82; Indels

Length 700;

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69 YDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKI-HDVLG 127
                                                                                                                                                                                                                                    129 DARRPADAHPVVGQRAF-QATLAQR-----QVTVATAAAGGRLALAAAGDVAQHRTQY 180
                                                                                                                                                                                                                                                                                                                                                                                    DVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATADALV---TDF
                                                                                                                                                                                                                                                                                                                    181 AEHQDQDEQHAEHLLDDVPEPRLRVERNAVDLFGLGRGERRVDHADAVAAAGVVAHRVL-
                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                              128 LGPDVYLGAYTRYYTGLLDALAD-----DV----
                                                                                                                ; Score 80.5; DE; Pred. No. 1.8; 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32970, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                             160 -AAAAVDELVARFLPMLKL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 VVAGGLVALVGRVRRQLRL 313
                   ; LENGTH: 700
; TYPE: PP F
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19384
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                                                                                                                  8.6%;
24.6%;
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                                                                                                                    Query Match
Best Local Similarity 24.6%
Matches 49; Conservative
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Best Local Similarity
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US-09-252-991A-32970
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SEQ ID NO 19384
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Facture No. 6551795

GENERAL INFORMATION:
FAPLICATION:
MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30019
LENGTH 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARPLICANT: MARCA J. RUBERFIELD Et al.
APPLICANT: MARCA J. RUBERFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PAPLICATION NUMBER: US 60/094,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1129 R-PFEVERFVGQR-----LHAVVGLGHLGGVEGVGLEDVGAGV----EVGLLDGL-DHVRA 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 RGEYDTEYAAQRARIGKIHDVLGLG------PDVYLGAYTRYYTGLLDALADDVVA 154
                                              63 ALVID---FYDHLESYERIQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQR--A 117
                                                                                                                                       241 RSG------GHTVIVG-----GRIERVLDRLRAGERLGTLLTPDRSRKAAR--KQW 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SNDNDTLVTAD-VRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEAT
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                                                                                                         RIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
8.7%; Score 81.5; DE
Best Local Similarity 22.5%; Pred. No. 3.4;
Matches 48; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19384, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30019
                                                                                                                                                                                       168 VARFLPMLKLLTFD 181
                                                                                                                                                                                                                              284 LAGHLOMRGTLVLD 297
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US-09-252-991A-19384
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GENERAL INFORMATION:
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APPLICATION
APPLICATION
APPLICATION
TITLE OF INVERTION:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 HALADRI-----GLDEREIAWRLSFTGIDDDTWAALAAEQPLFEATADALVTDFYDHLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 80; DB 4; Length 553; 21.1%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Mismatches
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US-09-252-991A-18102
; Sequence 18102, Application US/09252991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 AAQRARIGKIHDVLGLGPDVYLGA-----YTRYYT--GLLDALADDVVADRGEEAAAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Nagadara, Ayumu
TITLE OF INVENTION: Pyruvate Orthophosphate Dikinase Gene,
TITLE OF INVENTION: Recombinant DNA, and Process For Producing Pyruvate
TITLE OF INVENTION: Orthophosphate Dikinase
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DHLESYERTQDLFANSTKTVEQLKETQAEYLLGL--GRGEY-----DTEY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 LADRIGLDEAEIAWRLSFTGID-----DDTMAALAAEQ-----PLFEATADA--LVTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIRAKI-03009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/941,936
FILING DATE: 01-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      Sequence 2, Application US/08941936
Patent No. 6054305
GENERAL INFORMATION:
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                                                                                                                             APPLICANT: Tatsumi, Hiroki
APPLICANT: Eisaki, Naoki
APPLICANT: Horiuchi, Tatsuo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : |:
501 LGEVPVTASPVARY 514
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415-397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                              STREET: 220 mc. CTTY: San Francisco
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Best Local Similarity
Matches 49; Conserv
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                                                   JS-08-941-936-2
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                   Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 TDFYDHLESYERTQDLFANSTKTVEQ-----LKETQAEYLL-GLGRGEYDTEYAAQRARI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 IDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATADALVTDFYDHLESYE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 A-----LYESPRDYLAG--KSVEEKETYLAKTSYRDYLLKNVGLSETSVKYFQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 80; DB 4; Length 677;
; Pred. No. 2;
18; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 TG----MKDNKFGISHEQAVAAY--VYAHHLPNLKIVGIDCHI 226
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              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO A.
TITLE OF INVENTION: AERUCINOSA FOR DIAGNOSTI.
FILLE REFERENCE: 10/196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
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23.8%; Pred. No. 1.4;
ive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2595, Application US/09540236
Patent No. 6673910
                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                Query Match 8.6%;
Best Local Similarity 26.6%;
Matches 45; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.84
Matches 53, Conservative
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; ORGANISM: M.catarrhalis
US-09-540-236-2595
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GENERAL INFORMATION:
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US-09-540-236-2595
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Gaps

37;

Length 755; 73; Indels

DB 5;

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88 TVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                       678 MSRAENFKQVEYLLIHGTAD-DNVHFQQSAQISKA--LVDVGVDFQAMWYTDEDHGIASS 734
                                                                                                                                                                                                                                                                                                                                                                          618 WSYGGYVTSMVLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTV 677
                                                                                                                                                                                                                                                                                                                                                  46 -----TMAALAAEQPLFE---ATA-----DALVTDFYDHLESYERTQDLFANSTK
                                                                                                                                                                                                                                                                                                               558 STENIIVASFDGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRIAIWG
                                                                                                                                                                                                                                                                     2 SNDNDTLVTADVR-NGIDG----HALADRIGL----DEAEIAWRLSFTGIDDD-
                                                                                                                                                                                              Score 78.5; DB
Pred. No. 3.5;
5; Mismatches
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                                                                                                                                                                                              Query Match
Best Local Similarity 25.8%;
Matches 47; Conservative 2
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 755
    (617) 542-8906
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                                                                                                   TYPE: amino STRANDEDNESS:
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PCT-US93-07923-3
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 733
                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 LGAY-----TRYYTGLLDALADDVVADRGE-----EAAAAVDELVARFLPMLKLLT 179
                                                                                                                                                                                                                                                                                                                                                  223 IPAAVDNISSNYSVAERGKLTGILG------LNYQGYDKEHITQVLNAILVTYGAQN 273
                                                                                                                                                                                                                                                                                                                                                                                                                         -----ARIGKIHDVLGLGPDV---Y 133
                                                                                                                                                                                                                                                                                                                     ----TMAALA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 AEQPLFEAT----ADALVTDFYDHLESYERTQDLFANSTKTVE---------
                                                                                                                                                                                                                                                                                 83; Gaps
                                                                                                                                                                                                                                        Length 733;
                                                                                                                                                                                                                                                                                 74; Indels
                                                                                                                                                                                                                                                                                                                     9 VTADVRNGIDGHALADR-----IGLDEAEIAWRLSFTGIDDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9307923
GENERAL INFORMATION:
APPLICANT: Morimoto, Chikao
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: 3.5" Diskette, 1.44 Mb
IBM PS/2 Model 50Z or 55SX
SYSTEM: IBM P.C. DOS (Version 3.30)
                                                                                                                                                                                                                                          Score 78.5; DB 4;
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                 32: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,162
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/832,211
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
TRLECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 ----OLKETQAEYLLGLGRGEYDTEYAAQR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
OPERATING SYSTEM: IBM P.C. DUS NOTES OFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FITTING DATE: 19930819
                                                                                                                                                                                    GRGANISM: Acinetobacter baumannii US-09-328-352-5599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Fish & Richardsor
225 Franklin Street
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.6%;
Matches 52; Conservative 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
COMPUTER: IBM PS/2 M
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STATE: Massac
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PCT-US93-07923-3
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Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

August 10, 2004, 15:28:46; Search time 26.7312 Seconds

(without alignments)

Perfect score:

186-09-455-978B-77

Perfect score:

187-184 Million cell updates/sec

Title:

188-09-455-978B-77

Perfect score:

189-184 Million cell updates/sec

Title:

199-185-184 Million cell updates/sec

199-180-190-10.0, Gapext 0.5

Searched:

1291235 segs, 313682936 residues

Total number of hits satisfying chosen parameters:

1291235

Millium DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Millium Match 03*

Millium Match 03*

Millium Match 04*

Isting first 45 summaries

Database:

Published Applications AA:*

1 / Cap2_6/prodata/2/pubpa4/USO7_PUBCOMB.pep:*

2 / Cap2_6/prodata/2/pubpa4/USO7_BuBCOMB.pep:*

2 / Cap2_6/prodata/2/pubpa4/USO8_BuBCOMB.pep:*

3 / Cap2_6/prodata/2/pubpa4/USO8_BuBCOMB.pep:*

4 / Cap2_6/prodata/2/pubpa4/USO8_BuBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		1	563	18	480	602	US-10-282-122A-65364	7.5	10	2010	335	966	593	100	TG = 10 - 200 - 100 N - 000 00	, ,	989	JS-10-282-122A-61978	
		4-5	3-18	1-92	1-13	2A-6	2A-6	7-13			1-11	2A-5	4-72	4-48			4-48	2A-6	
ES			-49	92-9	-76	-12	-12	196-	, ,	4 6	9/-1	-12	-11	111	10	7	-11	-12	
SUMMARIES	1	-46(-369	-156	-156	-282	-283	-43	200	1 .	-156	-282	-425	-425		7 6	-425	-282	
SUS		US-10-460-524-5	US-10-369-493-18563	JS-10-156-761-9281	JS-10-156-761-13480	3-10	3-10	3-10	1 - 1	1 6	0T-0	3-10	US-10-425-114-72593	US-10-425-114-48921	1 -		JS-10-425-114-48636	3-10	
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	Score	66	94.5	94	89.5	88	87	86	85	2,	, ,	33.5	3.5	3.5	83.5	0	ה פ	62.5	
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	ult No.	П	7	m	4	S	9	7	œ	σ	1	0 1	11	12	13	14	۲ L	12	
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Sequence	Sequence	Semience	Segmence	Semente	Segment	Semience	Segmence	Sememen	Seguence	Segmence	Seguence	Segmence	Seguence	Segnence	Segmence	Segmence	Segmence	Sequence	Segmence	Sequence	Seguence	Seguence	Seguence	Segmence	Semente	Secretarion	Semience	Sequence	Sequence
US-10-282-122A-69832	US-10-369-493-13529	9-738-62	10-282-1	156-761-12605	10-425-114-6389	L0-289-456-16	10-622-064-2	10-243-739-	1-065-1	10-289-45	0-346-190-1	10-465-811	ᅼ	-10-6	10-050-902-2	-10-050-	10-369-493-1	10-282-122A-555	2-122A-6	128-7	US-10-369-493-8893	US-10-369-493-11290	-59	9-1	9-161	7-963-17142	2-122A-6977	82-122A-6213	US-10-437-963-184684
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б	765	831	928	939	318	329	329	329	329	329	329	329	329	329	330	330	901	1333	2799	1178	546	1173	2132	2151	2221	811	954	429	1015
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	1
US-10-4 ; Seque ; Publi ; GENER ; APPL	. 4 X K H
APPL ; APPL ; TITL ; FILE	APPLICANT: Brockle, lan APPLICANT: Brockle, lan TITLE OF INVENTION: Affinity Peptides and Method for Purification of Recombinant Prote TITLE SAM 743.11
CURR ; PRIO ; PRIO ; NUMB	CURRENT FILING DATE: 0203-06-12 PRIOR APPLICATION NUMBER: US 60/388,059 PRIOR FILING DATE: 2002-06-12 NUMBER OF SEQ ID NOS: 23
SEQ I	SOFTWARE: Patentin version 3.1 SOFTWARE: PATENTIN VERSION 3.1 SENTER: 448 TYPE: PRT
; ORG. US-10-4	; ORGANISM: Streptococcus US-10-460-524-5
Query Ma Best Loc Matches	Query Match 10.6%; Score 99; DB 12; Length 448; Best Local Similarity 25.3%; Pred. No. 0.087; Matches 48; Conservative 25; Mismatches 45; Indels 72; Gaps 8;
ò	10 TADVRNGIDGHALADRIGLDFAEIAWRLSFTGIDDDTWAALAAE 53
qa	41 TPIIRNGGELTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAAAWEA 97
ò	54QPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
QQ	98 AAAADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVV 145
δ	103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLPALADDVVADRGEEAAA 162
Db	146ESAKKARISEATDGLSDFLKSQTPAEDTVK 175

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100 LLG--LGRGEYDTEYAAQRA----RIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 TODLFANSTKTVEQ-----LKETQAEYLLGLGRGEYDTEYAAQRARIGKIHD--VLGL 128
                                                                                                                                                                                                                           82 TR-LKPNRRRYTQQEIADGAGMSRQQAGALIN-GDRRPTWEHCDAIQRFFRVHAGFLTAE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 IDDDTMAALAAEQPLFEATADALVTDFYDHLESY--ERTQDLFANSTKTVEQLKETQAEY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LSEQSAATVRATLPAVGAAVGEITARFYDRLFAARPELLRDLFNRG-----NQAAGTCRQA
                                                                                                                   25 ALADRIGVAHAEVFDVGRLSVASGVPEPVVKALLSGRPAGEPDLQA---RFLQRLDLRR
                                                                                      21 ALADRIGLDEAEI--AWRLSF-TGIDDDTWAALAAEQPLFEATADALVTDFYDHLESYER
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                                           22;
DB 14; Length 218; 0.11;
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                                                                                                                                                                                                                                                                                                        140 DPEALAGTLORSEQELLOQL-----ADRERAAMAVDDPLERLL 178
                                                                                                                                                                                                                                                                              129 GPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / match 9.6%; Score 89.5; DB Local Similarity 26.7%; Pred. No. 0.78; hes 36; Conservative 16; Mismarchae
                                             22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHIRA, TADANOSHI
APPLICANT: SHIRA, TADANOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
SEQ ID NO 13480
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13460. Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: SHIKAMA, HROSHI
APPLICANT: SHIBA, TADAXOSHI
  10.1%; Score 94; 28.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 66025, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Streptomyces avermitilis
US-10-156-761-13480
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 T----PEVÄÄÄWDEV 128
    Query Match
Best Local Similarity 28.7%
Matches 47; Conservative
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US-10-282-122A-66025
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                                                                                                                                                     Sequence 18653, Application US/10369493
; Sequence 18653, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: CAPE, Yongweiry J.
    APPLICANT: Gldman, Barry S.
    APPLICANT: Gldman, Barry S.
    APPLICANT: Chen, Xianfeng TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION: UNMBER: US/10/369,493
    CURRENT FILING DATE: 2003-02-28
    PRIOR PRILING DATE: 2003-02-21
    NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 RIGKIHDV-----LGL-GPDVYLGAYTRYYTGLLDALAD--DVVADRGEEAAAAVDEL 167
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10.1%; Score 94.5; DB 15;
Best Local Similarity 28.3%; Pred. No. 0.67;
Matches 51; Conservative 23; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9281, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIRAY, TADAYOSHI
APPLICANT: SHIRAY, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, WASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NOWBER 105/10/156,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9281
LENGTH: 218
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-9281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Halobacterium sp. NRC-1
                                                176 SIELAEAKVL 185
              163 AVDELVARFL 172
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IIILE OF INVENTION: Identification of Essential Genes in Microorganisms
                             CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-29
PRIOR PLILING DATE: 2000-05-29
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 AAEEKLGEVSDDMRNLEGVDADMLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-282-122A-65364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-437-963-137315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 --EATADALVIDFYDHLE--SYERTODLFANSTKIVEQLKETQAEYLLGLGRGEYDIEYA 113
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                                                                                                                                                                                                  FILE REFERENCE: ELITRA 0.34A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-21

PRIOR PILING DATE: 2000-05-22

PRIOR PILING DATE: 2000-05-22

PRIOR PILING DATE: 2000-05-22

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/25,625

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

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PRIOR PILING DATE: 2000-12-29

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PRIOR PILING DATE: 2000-12-29

PRIOR PILING DATE: 2000-12-29

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SE0 ID NOS: 78614
                                                                                                                                                       APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 DTLVTADVRNGIDGHALADRIGLDEAEIAWRLSF----TGIDDDTMAALAAEQPLF----
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9.4%; Score 88; DB 12; Length 505;
Best Local Similarity 25.7%; Pred. No. 1.5;
Matches 46; Conservative 24; Mismatches 69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 AAEEKLGEVSDDMRNLEGIDAD-
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haelbeck, Robert
APPLICANT: Ohleen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn version 3.1
                             Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NOS: 78614
Wall, Daniel
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APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Wa, Wei
APPLICANT: Wa, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBACE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 137315
LENGTH: 36-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 DRLALAIGRGGONVRLASDLTG------WOLNIMTSAEADERNAAEDAAIRRLFMNHLN 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 VDEETADVLVQEGFATLEEVAYVPAAELLA-----IEGFDEEIVDMLRNRARDAILTMAI 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 AQRARIGKIHDVL----GLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELV 168
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Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 DTLVTADVRNGIDGHALADRIGLDEAEIAWRLSF---TGIDDDTMAALAAEQPLF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.3%; Score 87; DB 12; Best Local Similarity 25.7%; Pred. No. 1.9; Matches 46; Conservative 24; Mismatches 69
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72;

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2211 KNSFDKDAVAKEINLOREVTKEFGRNAAQAVAAVADKLGNTOSYERYOEA---RTILLEAE 2267
                                                                                                                                                                                                                                                                                                                                                            -----AEKAAFRASLGQVNAYLAENQSRYDTWKEGGIGRSILHGAAG 2316
                                                                                                                                                                                                                                                                                                               LKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVL------GLGPDVYLGAYT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 FYDHLESYE-----RTQDLFANSTKTVEQLKE-TQAEYLLGLGRGEYDTEYAAQRARIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATADALVTD
                                                                                                                                                                                                                       ATADALVTDFYDHLESYERTQDLFANSTKTVEQ
                                                                                                                               3 NDNDTLVTADVRNGIDGHAL-----ADRIGLDEAEIAWRLSFTGIDDDT
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                                          Length 2703;
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                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2317 GLTIGSLGGILAGGGTSLAAPYLDKAAENLGPAGKAAVNAL 2357
                                                                                                                                                                                                                                                                                                                                                                                                           -ADDVVADRGEEAAAAVDEL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%; Score 83.5; DB 14;
24.1%; Pred. No. 1.9;
                                          DB 12;
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                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                          9.1%; Score 85; 23.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 DRG---EEAAAVDELVARFLPM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 DPGADPEETARALSELYGRIVPL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11335, Application US/10156761 publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), ORGANISM: Streptomyces avermitilis US-10-156-761-11335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KIHDVLGLGPDVYLGAYT----
                                                                                       26;
                                                                                                                                                                                                                            47 -----MAALAAEOPLFE--
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Best Local Similarity 24.1%
Matches 49; Conservative
                                                                                          52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         139 RYYTGLLDAL----
                                                                                                                                                                                                                                                                                                                                                              2268 LQNTDSE---
                                                                  Sest Local Similarity
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US-10-282-122A-59961
US-10-282-122A-66108
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LENGTH: 258
                                                                                                                                                                                                                                                                                                                      92
                                          Query Match
                                                                                          Matches
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                                                                                                                                                                                                                                                                           -----ERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEY 112
                                                                                                                                                                                                                                                                                                                                                                   AAQRARIGKIHDVLGLG-----PDVYLGAYTRY----YTGLLDALADDVVAD-- 155
                                                                                                                                                                                                                  8 LVTADVRNGIDGHALADRIGLDEAEIAWR----LSFT--GIDDDTMAALAAEQPLFEATA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
                                                                                            9.2%; Score 86; DB 16; Length 362; 26.4%; Pred. No. 1.6; Live 20; Mismatches 78; Indels
    ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3880C.1.pep
US-10-437-963-137315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66108, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: 60/206, 848
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/20, 335
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-12-02
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                                                                                                                           Conservative
                                                                                                                 Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                              62
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                                                                                                 Query Match
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CURRENT PLEA KERKENCE: ELITRA.034A

CURRENT PILING DATE: 2003-0.20

FRIOR APPLICATION NUMBER: 60/191,078

FRIOR PILING DATE: 2000-0.9-21

FRIOR PELING DATE: 2000-0.5-23

FRIOR FILING DATE: 2000-0.5-23

FRIOR FILING DATE: 2000-0.5-26

FRIOR FILING DATE: 2000-0.5-26

FRIOR FILING DATE: 2000-0.5-26

FRIOR FILING DATE: 2000-0.9-0

FRIOR FILING DATE: 2000-0.9-0

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FRIOR FILING DATE: 2000-0.9-0

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FRIOR FILING DATE: 2000-12-23

FRIOR FILING DATE: 2000-12-22

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FRIOR FILING DATE: 2000-12-22

FRIOR FILING DATE: 2000-01-02-06

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FRIOR FILING DATE: 2001-02-16

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FRIOR FILING DATE: 2001-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Sequence 59961, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 ADDVVADRGEEAAAAVDELVA 169
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US-10-282-122A-59961
                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRA.034A
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Trawick, John
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; Sequence 72593, Application US/10425114 ; Publication No. US20040034888A1

US-10-425-114-72593

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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 ERTODLFANSTKTV-----EQLKETQAEYLLGLGR------GEYDTBYAAQ-----R 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 ARIGKIHDVLGLGPDV----YLGAYTRY---YTGLLDALADDVVADRGEEAAAAVDELVA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 GIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATADALVTDFYDHLESY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GIDGHALADRIGLDEAEIAWRLSFTGIDDDIMAALAAEQPLFEATADALVTDFYDHLESY 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

8.9%; Score 83.5; DB 12; Length
Best Local Similarity 25.3%; Pred. No. 3;
Matches 47; Conservative 24; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: CC-ZMPO14820017E02_FLI.pep
US-10-425-114-72593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: CC-ZMP0148032B07_FLI.pep
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25.3%; Pred. No. 3;
tive 24; Mismatches
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Publication No. US20040034888A1
GENERAL INFORMATION:
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311 SFEPLL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 RFLPML 175
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
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LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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152 GVDGRRVGLDBEAPADADAVAAQHRDHLLDVEALLVELVDELGH- 196	OPLFEATADAL
CHIEF TOE	DD 717 AGPQVQAAADSALKBGTPDALDEFVNGDGYEKARYLDQVQQAYELTDT 764
: HHVRALLLQ	102 GLGRGYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVAD
117 ARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVA 169	Db 765GGPEVQIAAEAAVTGDRQQLDEFVSIGQYRRAILDSQRDAHNAEINALLS 814
:	
170 RFLPML 175	Db 815 AGONAAELASQEAANAQEAYTRATGDAQ 842
311 SFEPLL 316	RESULT 14
RESULT 13	US-10-425-114-48636 Application US/10425114 ; Sequence 46836, Application US/10425114
US-10-282-122A-53778 Semience 53778, Application US/10282122A	GENERAL INCORMATION:
CPUDICATION NO. 0220040029129A1 CPUDICATION NO. 0220040029129A1	
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APPLICANI: Adminuto, Carlos APPLICANI: Malone, Cheryl	, APPLICANT: Tabaska, Jack E
	; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With , with OF INVENTION: Plants and Uses Thereof for Plant Improvement
APPLICANT: Zyskind, Judith APPLICANT: Wall. Daniel	
	MBEK: 2003-(
APPLICANT: Carr, Stant APPLICANT: Yamamoto, Robert	; NUMBER OF SEQ ID NOS: 73128 : SEQ ID NO 48636
APPLICANT: Forsyth, K. APPLICANT: Xu, H.	LENGTH: 384
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REPERENCE: RIJERA 034A	\mathbf{H}
CURRENT APPLICATION NUMBER: US/10/282,122A	; FEATURE: ; OTHER INFORMATION: Clone ID: LIB3116-002-B8_FLI.pep
CURRENT FILING DATE: Z003-02-20 PRIOR APPLICATION NUMBER: 60/191,078	-114-48636
PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848	1 8.9%; Score 83; DB 12; Length 384; cimilarity 25.6%; Pred. No. 3.6;
PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727	1; Conservative 25; Mismatches
PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/230,335	OY 58 BATADALVIDF-YDHLESYERIQDLFANSTKIVEQLKETQAEYLLGLGRGEYD 109
	Db 267 KANSDAPITAYRYHSLCSYMGDDDMF-SSDLSEDQLKQRLGHMSITQCQVIFSMG-DEYV 324
	Qy 110 TEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEFAAAAVDELVA 169
	325
FILING DATE: 2000-11-27	0,1 8 0,1
PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22	
APPLICATION NUMBER: FILING DATE: 2001-02	JD 5/3 K 5/3
	RESULT 15
	US-10-282-122A-61978 ; Sequence 61978, Application US/10282122A
NUMBER OF SEC ID NOS: 78813 SOFTWARE: PatentIn version 3.1	; Publication No. US20040029129A1
SEQ ID NO 53778 LENGTH: 1254	; APPLICANT: Wang Liangsu . a Dor I Cann. Carlos
TYPE: PRT ORGANISM: Cornyebacterium diptheriae	Malone, C
4-53778	
Query Match 8.9%; Score 83.5; DB 12; Lengtn 1254; Best Local Similarity 25.0%; Pred. No. 16; Matches 52; Conservative 23; Mismatches 82; Indels 51; Gaps 10;	APPLICANT: Wall, Daniel ; APPLICANT: Transick, John , Applicant: Transick, John
4 DNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTG 41	, APPLICANT: Yamamoto, Robert , APPLICANT: Forsyth, R.
658 DNLNLVNHWALFDPNEDLRNAADEAGYEDDITLDEFVNITAPQMRLPGLVKKAWELR-DG 716	2

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FILE REFERENCE: ELITRA.034A
CORRENT FALLIAGO DATE: 2003-02-20
FRIOR PRILIAG DATE: 4003-02-20
FRIOR PELIAGO DATE: 4000-03-21
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FRIOR PELIAG
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Search completed: August 10, 2004, 15:42:28 Job time: 27.7312 secs Blank

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GenCore version 5.1.6
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- protein search, using sw model OM protein

August 10, 2004, 15:22:45; Search time 8.01937 Seconds (without alignments) 2207.061 Million cell updates/sec Run on:

US-09-455-978B-77 933

Title: Perfect score: Sequence:

1 MSNDNDTLVTADVRNGIDGH........BELVARFLPMLKLLTFDQQI 184 Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Htrlo transfer	transducer protein	methyl-accepting o	methyl-accepting o	methyl-accepting o	methyl-accepting c	methyl-accenting c	methyl-accepting o	Igg-binding profei	profein G precureo	hypothetical prote	hypothetical prote	probable DNA2-NAM2	hypothetical prote	Two component gone	protoin general	procein sensor pro	Town binesis and a	M wet 1 fact on and	N utilication subs	n deitisacion subs		hypothetical prote	hemadalutinin/hemo	electron transfer	concorred himster	conserved hypothet	dag-mosicalo proto:	gas-vestore procer	readuntougn proces
SUMMARIES		E84304	T44978	A83713	C69832	C87302	A97485	AB2703	D87536	A24496	S00128	T35174	A84210	T00533	C84609	AD2580	292260	AH3535	A47334	B81060	H81816	T45238	B87094	F84349	H81193	C84365	F96022	S	·	S01964	2
	DB	2	7	7	~	7	7	7	7	N	7	~	~	~	7	α	2	~	2	· ^	۱ 🛚	N	~	~	7	7	2	N	(7	· C	2
	Length	489	489	439	432	537	499	499	555	448	593	218	883	1090	2048	881	881	503	955	500	505	775	469	157	2703	266	491	712	381	331	1
do	Query	100.0	100.0	15.9	15.2	14.1	$^{\circ}$	N	Н	0	0	0	0	10.1	0	10.0	10.0	6.6	9.5	4.6	9.4	4	9.3	9.3	9.1	9.1	0.6		8.8		
	Score	933	933	148	142	132	117.5	117.5	105.5	66	98	97	94.5	94	93.5	93	93	92.5	89	88	88	88	87	86.5	85	84.5	84	ω.	82.5	82	
	Result No.		7	е	4	2	9	7	80	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	

dlutamate 5-kinase	probable nicotine	gation transfer	carion-riansportin	nypothetical prote	hypothetical prote	translation initia	hypothetical prote	nrobable RNA-direc	hypothetical prote	transducer protein	Cobinamide kinase	hypotherical prote	hypothetical prote	hypothetical proto	Badiling anthradia	2,4-diaminobutyrat
G83074	D72530	20000	1000CH	199771	H84184	S74544	T08986	S58380	C84160	T44946	S52220	G82697	A83182	A95951	AE1139	F83720
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82 8.8 37								8.7						8.5	8.5	

ALIGNMENTS

RESULT 1	
E84304	
Htr10 transducer [imported] - Halobacterium sn NBC-1	
C; Species: Halobacterium sp. NRC-1	
C;Date: 02-Feb-2001 #sequence revision 02-Feb-2001 #rext change 16-Feb-2001	
C; Accession: E84304	
RiNg, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bermist, B.; Dan M.; Shikla H.D., Lack, C.	S transfer .
; Leithauser, B.; Keller, K.; Cruz. R.: Danson M. J. Hondh D. W. Maddack.	Table
Jung, K.H.; Alam, M.; Freitas, T.	יפיי משחדה
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000	
A, Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Rhhardt H. Iome T.M. T.;	
A)Title: Genome sequence of Halobacterium snecies NRC-1	. 1. C
A; Reference number: A84160; MUID: 20504483; PMID: 11016950	
A; Accession: E84304	
A;Status: preliminary	-
A; Molecule type: DNA	
A;Residues: 1-489 <sto></sto>	
A; Cross-references: GB: AE004437; NID: G10580997: PIDN: AAG19801 1. GGDD: CHARLO	
C;Genetics:	
A; Gene: htr10	

C, Superfamily: Halobacterium salinarum transducer protein htrl

Gaps .; 0 Length 489; Indels Query Match 100.0%; Score 933; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.9e-70; Matches 184; Conservative 0; Mismatches 0;

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61 ADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG 120 9 1 MSNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFBAT d à qq ò

KIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTF 180 121 g

DQQI 184 DQQI 184 181 181 δ 台

RESULT 2 T44978

transducer protein hemAT [validated] - Halobacterium salinarum
N;Alternate names: methyl-accepting taxis protein htB; transducer protein htB; transducer
C;Species: Halobacterium salinarum
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 15-Sep-2000
C;Accession: T44978
R;Zhang, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.
Proc. Natl. Acad. Sci. U.S.A. 93, 4649-4654, 1996

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A; Cross-references: GB: AE005673; NID: 913421593; PIDN: AAK22415.1; GSPDB: GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Superfamily: methyl-accepting chemotaxis protein mcpA
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Best Local Similarity
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Cipate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
Cipate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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Cipate: 01-Dec-2000 #sequence_revision 01-Dec-2000
Cipate: 01-Dec-2000 #sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83713
A; Reference number: A83713
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A; Reference number: A; Reference of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; R
A,Title: Signal transduction in the archaeon Halobacterium salinarium is processed throut A,Reference number: Z22804; MUID:96209786; PMID:8643458
A,Accession: T44978
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-489 <ZHA>
A,Cross-references: EMBL:U75436; NID:g1654420; PIDN:AAB17881.1; PID:g1654421
A,Reperimental source: strain Flx15
A,Note: the source is designated as Halobacterium salinarium
C,Genetics: And A,Gene: hemAT; htpl5; htb
C;Function:
A,Bescription: involved in aerotactic signal transduction; involved in oxygen sensing; mC;Superfamily: Halobacterium salinarum transducer protein htrl
C;Superfamily: Halobacterium salinarum transducer protein htrl
C;Keywords: heme; methylated amino acid; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methyl-accepting chemotaxis protein BH0505 [imported] - Bacillus halodurans (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --VRIGLQTKWYVSAFQQLT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADALVIDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIHDVIGIGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 933; DB 2;
100.0%; Pred. No. 1.9e-70;
ive 0; Mismatches 0;
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Best Local Similarity 25.2%; Pred. No. 8e-05;
Matches 39; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184; Conservative
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Best Local
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C; Accession: G69832
R; Kunst, F:; Ggasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc C; Accession: G69832
R; Kunst, F:; Ggasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Brulich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc A; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lavine, J.; Harwood, C.R.; Hanaut, A.; Hulbert, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Ee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel A; M.; Cgiwara, A.; Oudega, B.; Park, S.H.; Park, V.; Bohl, T.M.; Portetelle N; M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tosato, V.; Saco, T.; Sechowska, A.; Sero, A; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Artile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Artile: The complete genome cof the Gram-positive bacterium Bacillus subtilis. A; Artile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Artile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Artile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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C; Spate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C; Accession: C87302
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon D. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUD:21173699; PMID:11259647
A; Molecule type: DNA
A; Residues: 1-537 < STO.
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A;Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12878.1; PID:g2633374
A;Experimental source: strain 168
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                                                         C;Spēcies: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
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methyl-accepting chemotaxis protein homolog yhfv - Bacillus subtilis
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25.3%; Pred. No. 0.00025;
cive 29; Mismatches 76;
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3;

Gaps

12;

14.1%; Score 132; DB 2; Length 537; larity 27.2%; Pred. No. 0.0023; Conservative 26; Mismatches 72; Indels

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methyl-accepting chemotaxis protein McpM [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: O-Apr-2001
#sequence_revision 20-Apr-2001
#sequence_revision 20-Apr-2001
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, W.T.; DeBoy, R.T.; Dodson, R.J.; Burkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D, J.; Ermolaeva, M.; White, O.; Salzberg, S.D.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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R;Fahnestock, S.R.; Alexander, P.; Nagle, J.; Filpula, D.
Bacteriol. 167, 870-880, 1986
A;Title: Gene for an immunoglobulin-binding protein from a group G Streptococcus. A;Reference number: A24496; MUID:86304178; PMID:3745123
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J. Biol. Chem. 266, 399-405, 1991
A;Title: Streptococcal protein G. Gene structure and protein binding properties.
                                                                                                                                                                                                                                                                                                                         5
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C;Genetics:
                                                                                                                                                                                  78
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                                                                                                                                                                                                                   3 GQAKTDR-QLDE-----RLNFLGLGHGERQNLSDMKGVITGSLDASLDRFYTKVRAVPET
                                                                                                                                                                                                                                                                                        79 ODLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYT
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C;Species: Streptococcus sp.
C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 17-Mar-2000
                                                                                                                                                                         19 GHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERT
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                                                                                                                        7 ;
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                                                               Length 499;
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                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 --VAKRAKGLFNSAKSDAELADGLSALIKAAFLDMDLSVSTY 202
                                                         ch 12.6%; Score 117.5; DB 2; Similarity 26.5%; Pred. No. 0.034; 35; Conservative 23; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 105.5; DB llarity 24.7%; Pred. No. 0.39; Conservative 28; Mismatches
A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                        139 RYYTGLLDALAD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 LMLDGIVKAVIE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 DVVADRGE-----
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tes 40; Conserva
                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-555 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary A;Molecule type: DNA
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                                                         Query Match
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                                                                                       Best Loca
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
A97485
methyl-accepting chemotaxis protein mcpV (AF312877) [imported] - Agrobacterium tumefacie methyl-accepting chemotaxis protein mcpV (AF312877) [imported] - Agrobacterium tumefaciens of Species: Agrobacterium tumefaciens c.) and the sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C.) Accession: A97485
R)Goodner, B, Hinhikle, G, Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A)Fitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A)Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Accession: AB2703
R'Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. Klyood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; MUID:21608550; PMID:11743193
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                           KETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDV 152
                                                                                                                                                                            71 SROOAHWGV-IAEGOFSDDYVQAVRAIGOTHARIGLEPRWYIGGYAVVGDHLVRAVIDSM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-499 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86834.1; PID:g15156046; GSPDB:GN00169
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A;Cross-references: GB:AE008688; PIDN:AAL42040.1; PID:g17739417; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                 70
               IAWRLSFTGIDDDTWAALAABQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
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                                                            IGERTAFWGIDDKARSALRDLRPVIRÅEIGKALDNFYGKVRATPETRKFFSDDRHMNAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 QDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 GHALADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATADALVTDFYDHLESYERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GQAKTDR-QLDE----RLNFLGLGHGERQNLSDMKGVITGSLDASLDRFYTKVRAVPET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 117.5; DB 2; 26.5%; Pred. No. 0.034; tive 23; Mismatches 67;
                                                                                                                                                                                                                                                                                  130 WPRGLLAKGGSDRAGEAVAAL--MKAIFLDM 158
                                                                                                                                                                                                                                                    ------VADRGEEAAAAVDELVARFLPM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: AGR_C_1888
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 26.59
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:: |:: |
116 LMLDGIVKAVIE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 RYYTGLLDALAD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A97485
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
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A Molecule type: DNA
A, Molecule type: Lold eSEBS-
A, Cross-references: ESEBS-AL031107; PIDN:CAA19954.1; GSPDB:GN00070; SCOEDB:SC5A7.25c
A, Experimental source: strain A3(2)
C, Genetics: SCOEDB:SC5A7.25c
C, Superfamily: Streptomyces coelicolor hypothetical protein SC5A7.25c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 LV-TDFYDHLESYERTQDLFANSTKTVEQ-----LKETQAEYLLGLGRGEYDTEYAAQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----INNAKTVEGVKDLQAQVV-- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 ----QPLFEATADAL-----VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ESAKKARISEATD------GLSDFLKSQTPA---EDTVK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 DVQTRFVQRLDLLRRTR-LKPNGRKYTQQEIADGAGMSRQQAGALIN-GDRRPTMEHCDA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 RARIGKIHD--VLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEBAAAAVDELVARFL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 TPIIRNGGE----LTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAAAWEA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 TLVTADVRNGIDGHALADRIGLDEAEI--AWRLS-FTGIDDDTWAALAAEQPLFEATADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: T35174
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                          72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 218;
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                                                                                                                                                                                                                                                                                                                                                                              Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Indels
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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29.6%; Pred. No. 0.62;
tive 21; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 TADVRNGIDGHALADRIGLDEAEIAWRLSFIGIDD
                                                                                                                                                                                                                                                                                                                                                                              ch 10.5%; Score 98; DB 1 Similarity 25.3%; Pred. No. 1.8; 48; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 AAAADALAKAKADALKEFNKYGVSDYYKNL--
                                                                                                                                                                                                                                                                                              F,498-567/Domain: proline-rich <PRO>F,568-593/Domain: carboxyl-terminal <CTD>
                  F,192-215/Region: A repeat
F,216-266/Region: B
F;267-290/Region: A repeat
F;303-497/Domain: IgG binding <I
F;303-357/Region: C repeat
F;358-372/Region: C repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 AVDELVARFL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 SIELAEAKVL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: Z21570
                                                                                                                                                                                                                                                                  C repeat
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                   F;428-442/Region:
F;443-497/Region:
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Best Local S:
Matches 53
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C.Species: Streptococcus gp.
A.Varietey: Streptococcus gp.
A.Varietey: Streptococcus gp.
C.Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 19-May-2000
C.Accession: S00128; A27604; E26314 M. Second B.; Hellman, U.; Lindberg, M.; Uhlen, M.
Rur. J. Biochem. 168, 319-324, 1988
A.Fillse: Structure and evolution of the repetitive gene encoding streptococcal protein GA.Reference number: 800128; MUID:88029445; PMID:3665928
A.Accession: S00128; MUID:88029445; PMID:3665928
A.Accession: S00128; MUID:88029445; PMID:3665928
A.Accession: S00128; MUID:88029445; PMID:3665928
A.Accession: Solution of the repetitive gene encoding streptococcal protein GA.Reference number: 1593 - COLS.
A.Accession: Solution of the repetitive gene encoding streptococcal protein GA.Residues: 1-593 - COLS.
A.Accession: Solution of the repetition of the mature protein, was confir G. S.Gobring, U.; Falkenberg, C.; Nielsen, E.; Akerstroem, B.; Bjoerck, L.
S.Sicebring, U.; Falkenberg, C.; Nielsen, E.; Akerstroem, B.; Bjoerck, L.
S.Sicebring, U.; Falkenberg, C.; Nielsen, E.; Akerstroem, B.; Bjoerck, L.
A.Accession: A.Fresidues: 62-10, MUID:88154455; PMID:2831269
A.Atcession: A.Fresidues: 62-10, ASO,
A.Accession: A.Fresidues: 62-10, ASO,
A.Accession: A.Fresidues: 62-10, ASO,
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A.Accession: A.Fresidues: 62-10, ASO,
A.Accession: A.Fresidues: 114-40, ASO,
A.Accession: A.Fresidues: 62-10, ASO,
A.Accession: A.Fresidues: 62-10, ASO,
A.Accession: A.Fresidues: 62-10, ASO,
A.Accession: A.Fresidues: 62-10, ASO,
A.Accession: A.Fresidues: 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
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                                                                                                                                                                                                                                                                                                                                                                                                                       10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD-----DTWAALAAE----
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                                                                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein G precursor - Streptococcus sp. (Streptococcus G148)
N;Alternate names: albumin-binding protein; cell wall-bound protein
                                                                                                                                                                                                                                                                                                 DB 2; Length 448;
                                                                                                                                                                                                                                                                                                                                                               45; Indels
A; Reference number: A39041; MUID: 91093154; PMID: 1985908
                                                                                                                                                                                                                                                                                                 Query Match 10.6%; Score 99; DB 2
Best Local Similarity 25.3%; Pred. No. 1;
Matches 48; Conservative 25; Mismatches
                           A,Accession: A39041
A,Status: preliminary
A,Molecule type: protein
A,Residues: 34-42,'N',45-48,62-76,186-200 <SJO>
C,Genetics:
A,Gene: psp C,Superfamily: M5 protein
C,Superfamily: M5 protein
C,Keywords: transmembrane protein
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1117-290/Domain: AB duplication <DUPl>
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176 SIELAEAKVL 185
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99

Gaps

550

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hypothetical protein At2g22130 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (accession: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (Specession: C84669 (Species) (Specession: C84669 (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (Species) (S
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            two component sensor kinase Atu0027 [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1414 LHEAISRALVKLGKDRPACKLEMVKAGVIDCVLDILHEAPDFLCAAFSE----LLRILTN 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | : | : | : | : | : | 419 | 441 PSYEEQTPATPDCFTTSFVDHLHRSFNAPQLAAIHWAAMHTAAGTSSGVKK-QEPWPFTL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 LFEATADALVIDFYDHLESYERTQDLFANSTKTVEQLKETQAEY-----LLGLGRGE-YD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------IHDVLGLGPDVYLGAYTRYYTGLLDALAD 150
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-881 «KUR»
A;Cross-references: GB:AE008688; PIDN:AAL41058.1; PID:g17738345; GSPDB:GN00186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: GB:AE002093; NID:g6598689; PIDN:AAF18668.1; GSPDB:GN00139
                                                                                                                                                                                                                     --GKTHTVWGMLNVIHLVQYQQYYTSLLKKLAPETYNQANECSSSD
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD2580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 2048;
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                                                                                                                                               104 GRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALA-
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26.3%; Pred. No. 20;
cive 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                             151 DVVADRGEEAAAVDELVARFLPMLKLLT
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A;Molecule type: DNA
A;Residues: 1-2048 <STO>
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Matches
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84210
R;Accession: A84210
R;NG; W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablq Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Recession: A84210
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-883 <STO>
A;Cross-references: GB:AE004437; NID:g10580117; PIDN:AAG19045.1; GSPDB:GN00138
C;Genetics:
A;Genetics:
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A.Kross-references: EMBL:AC002392; NID:g3176701; PID:g3176714

A.Kross-references: EMBL:AC002392; NID:g3176701; PID:g3176714

A.Kross-references: Enditivar Columbia

B.Experimental Source: cultivar Columbia

R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable DNA2-NAM7 helicase family protein [imported] - Arabidopsis thaliana N'Alternate names: SEN1 protein homolog T20K24.14 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001 C;Accession: T00533; G84572 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, B;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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A,Molecule type: DNA
A,Residues: 1-1090 <STO>
A,Cross-references: GB:AE002093; NID:g3176714; PIDN:AAD12029.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVRNGIDGH--ALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEA-----TAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%; Score 94.5; DB 2; Length 88: 28.3%; Pred. No. 5.8; ive 23; Mismatches 63; Indels
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A;Introns: 250/1; 310/1; 342/1; 383/2; 427/3; 1016/3
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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                                                                     ADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGBYDTBYAAQRARIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96209786; PubMed=8643458; Zhang W.; Brooun A., McCandless J., Banda P., Alam M.; Zhang W. Brooun A., inclandess J. Banda P., Alam M.; Signal transduction in the archaeon Halobacterium salinarium is processed through three subfamilies of 13 soluble and membrane-bound
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MEDLINE=20140131; PubMed=10676961;
Hou S., Larsen R.W., Boudko D., Riley C.W., Karatan B., Zimmer M.,
Ordal G.W., Alam M.;
"Myoglobin-like aerotaxis transducers in Archaea and Bacteria.";
Nature 403:540-544(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Heme-containing signal transducer responsible for aerotaxis, the migratory response toward or away from oxygen.
--- SUBUNIT: Homotetramer (Probable).
--- SIMILARITY: Contains 1 methyl-accepting transducer domain.
                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heme-based aerotactic transducer hemAT (Transducer HtB protein).
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GO; GO:0020037; F:heme binding; IDA.

GO; GO:0004871; F:signal transducer activity; IDA.

GO; GO:0004454; P:serotaxis; IDA.

GO; GO:0007165; P:signal transduction; IDA.

InterPro; IPR004099; Chmtaxis_transd.

InterPro; IPR004099; Me chemotaxis.

PFR0015; MCPsignal; 1.
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Proc. Natl. Acad. Sci. U.S.A. 93:4649-4654(1996).
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Borriss R., Boursier L., Brans A., Braun M., Brighell S.C., Bron S.,
Bruschier L., Brans A., Braun O., Carter N.M.,
A broilet S., Bruschi C.V., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F., Deviner K.M., Dusterhoft A., Erhilch S.D., Bamerson P.T.,
A briz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,
A chims S.Y., Glaser P., Goffeau A., Gollghtly B.J., Arandat D.,
A duiseppi G., Guy B.J., Hajech J., Harwood C.R., Henaut A.,
A tlibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A chims S.Y., Coatter P., Koningstein G., Krogh S., Kumano M.,
A kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A kobayashi Y., Lardinois S., Lauber J., Lazarevic V.,
A Medina N., Mellado R.P., Mizun M., Moselt D., Nakai S., Noback M.,
A Moone D., Orbailly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Presecan E., Pujic P., Purnelle D., Porwollik S., Rey M., Reynolds S.,
A Rieger M., Rivolta C., Rocha E., Roche M., Sadaie Y.,
A Rieger M., Rivolta C., Roche B., Roche P., Rochfone F.,
A Rieger M., Rivolta C., Roche B., Roche P., Rochfone F.,
                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                 121 KIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEBAAAAVDELVARFLPMLKLLTF 180
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                                                                                                                                                      Gaps
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                                                                                                                                                      .
0
                                                                                             DB 1; Length 489;
454 METHYL-ACCEPTING TRANSDUCER.
52816 MW; 8457263FCF616BFF CRC64;
                                                                                                                                                      Indels
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NCBI_TaxID=1423;
                                                                                          100.0%; Score 933; DB 1;
100.0%; Pred. No. 4.1e-68;
Live 0; Mismatches 0;
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Last annotation update)
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10-OCT-2003 (Rel. 42, Last annotation u
Heme-based aerotactic transducer hemAT.
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                                                                                                                                                            Conservative
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                                     489 AA;
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Bacillus subtilis.
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                                        SEQUENCE
                                                                                                Query Match
                                                                                                                                      Local
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)1-JAN-1988 (Rel. 06, Created)
)1-JAN-1988 (Rel. 06, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Immunoglobulin G binding protein G precursor (IgG binding protein G)

01-JAN-1988

448 AA.

STANDARD;

SPG1_STRSG P06654;

Streptococcus sp. (Lancefield group G). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

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Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambut R., Wedler B., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."
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                                                                                                                                                                                                                                      MEDLINE=20140131; PubMed=10676961;
Hou S., Larsen R.W., Boudko D., Riley C.W., Karatan B., Zimmer M.,
Ordal G.W., Alam M.;
"Myoglobin-like aerotaxis transducers in Archaea and Bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  *Resonance Raman and ligand binding studies of the oxygen-sensing signal transducer protein HemAT from Bacillus subtilis.";
J. Biol. Chem. 277:13528-13538 (2002).
-!- FUNCTION: Heme-containing signal transducer responsible for aerotaxis, the migratory response toward or away from oxygen.
-!- SUBUNIT: Homotetramer (Probable).
-!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21950695; PubMed=11821422;
Aono S., Kato T., Matsuki M., Nakajima H., Ohta T., Uchida T.,
Kitagawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.2%; Score 142; DB 1; Length 432; 25.3%; Pred. No. 0.00027; Live 29; Mismatches 76; Indels
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GO; GO:0004871; F:signal transducer activity; IDA.
GO; GO:0009454; P:aerotaxis; IDA.
GO; GO:0007165; P:signal transduction; IDA.
InterPro; IPR004089; Chmtaxis transd.
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Transducer; Heme; Complete proteome.
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RESONANCE RAMAN SPECTROSCOPY, AND SUBUNIT.
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EMBL; Z99109; CAB12878.1; -.
PIR; C69832; C69832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00015; MCPsignal; 1.
SMART; SM00283; MA; 1.
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SubtiList; BG13066; hemAT.
                                                                                                                                                                               Nature 390:249-256(1997).
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Local Sım.
~ 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91335209; PubMed=1871600;
Gronenborn A.M., Filpula D.R., Essig N.Z., Achari A., Whitlow M., Wingfaled P.T., Clore G.M.;
"A novel, highly stable fold of the immunoglobulin binding domain streptococcal protein G.";
Science 253:657-661(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M13825; AAA03664.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1EM7; 08-MAY-02
1FCC; 20-JUL-95
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PDB; 1EM7; 08-MAY-02
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1IGD;
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PDB;
PDB;
PDB;
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151 DVVADRGEEAAAAVDELVARFLPMLKLLTFDQQI 184 -----EASITNQQELLKAIKATTKILNLEQQL 175

149

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RESULT 4 SPG1_STRSG

X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 228-282. Butterworth S., Lamzin V.S., Wigley D.B., Derrick J.P., Wilson K.S.; Submitted (APR-1997) to the PDB data bank.

STRUCTURE BY NMR OF 298-351

Sauer-Eriksson A.E., Kleywegt G.J., Uhlen M., Jones T.A.; "Crystal structure of the C2 fragment of streptococcal protein G in complex with the Fc domain of human IgG."; Structure 3:265-278(1995).

K-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 297-352.

complex with Fab."; J. Mol. Biol. 243:906-918(1994)

MEDLINE=95308043; PubMed=7788293;

in a

Derrick J.P., Wigley D.B.;
"The third 16G-binding domain from streptococcal protein G. A analysis by X-ray crystallography of the structure alone and complex with Fab.";

X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 293-351. MEDLINE=95055731; Pubmed=7966308;

immunoglobulin-binding domain

Gallagher T., Alexander P., Eryan, P., Gilliland G.L.
"Two crystal structures of the B1 immunoglobulin.bin
Bireptococcal protein G and comparison with NMR.";
Biochemistry 33:4721-4722(1994).

(2.07 ANGSTROMS) OF 228-282.

MEDLINE=94213848; PubMed=8161530;

X-RAY CRYSTALLOGRAPHY

streptococcus."; J. Bacteriol. 167:870-880(1986)

Φ

MEDLINE=86304178; PubMed=3745123; Fahnestock S.R., Alexander P., Nagle J., Filpula D.; "Gene for an immunoglobulin-binding protein from a group

SEQUENCE FROM N.A. NCBI_TaxID=1320;

593 AA

PRT;

STANDARD;

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SPG2_ST
P19909;
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----QPLFEATADAL-----VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----INNAKTVEGIKDLQAQVV--
                                                                                                    Pfam; PF00746; Gram pos_anchor; 1.
Pfam; PF00746; Gram pos_anchor; 1.
Pfam; PF01459; IgG binding B; 2.
Pfam; PF04650; XSTRK signal; 1.
PRINTS; PR00015; GPOSANCHOR.
TIGRFAMS; TIGR01167; LPXTG anchor; 1.
TIGRFAMS; TIGR01167; LSXTS signal; 1.
PROSITE; PS50847; GRAM POS_ANCHORING; 1.
IgG-binding protein; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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5 X 5 AA REPEATS OF [DE]-D-A-K-K.

LPXTG SORTING SIGNAL (POTENTIAL).

AMIDE-LINKED TO CELL WALL (POTENTIAL).
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                                                                                                                                                                                                                                                                  55 AA REPEATS.
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                                                                                                                                                                                                                                     X 37 AA REPEATS
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                             PDB; 1PGX; 15-JUL-92.
PDB; 2GB1; 15-APR-93.
PDB; 21GD; 29-JUL-94.
PDB; 21GH; 31-JAN-94.
InterPro; 1PR002988; GA.
InterPro; IPR001999; Gram pos_anchor.
InterPro; IPR001999; Gram pos_anchor.
InterPro; IPR001999; Gram pos_anchor.
Pfam; PP01468; GA; 2.
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448 AA;
            30-APR-94
                      30-APR-94
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1PGB;
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SPG2_STRSG

RESULT 5

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                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GX7805;
MEDLINE=88015586; PubMed=3658689;
Filpula D., Alexander P., Fahnestock S.R.;
"Nucleotide sequence of the protein G gene from Streptococcus GX7805,
and comparison to previously reported sequences.";
Nucleic Acids Res. 15:7210-7210(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Struct, Biol. 5:470-475(1998).
-!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
                         01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Immunoglobulin G binding protein G precursor (IgG binding protein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-86500657; PubMed=3017704; Guss B., Elasson M., Olsson A., Uhlen M., Frej A.-K., Joernvall H., Plock J.-I., Lindberg M.; Structure of the IgG-binding regions of streptococcal protein G."; EMBO J. 5:1567-1575(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malakauskas S.M., Mayo S.L., mipsign, structure and stability of a hyperthermophilic protein variant. ";
                                                                                                                                                                                                                                                 Olsson A., Eliasson M., Guss B., Nilsson B., Hellman U.,
Lindberg M., Uhlen M.;
                                                                                                                                                                                                                                                                                    "Structure and evolution of the repetitive gene encoding streptococcal protein G.";
                                                                                                           Streptococcus sp. (Lancefield group G).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S00128; S00128.

PDB; 1GB4; 22-JUL-98.

PDB; 1FCC; 20-JUL-95.

PDB; 1FCC; 19-SEP-01.

PDB; 1GJ5; 21-MAR-02.

PDB; 1GJ7; 09-AMG-01.

PDB; 21GG7; 09-AMG-01.

PDB; 21GG7; 09-AMG-01.

PDB; 21GG7; 09-AMG-01.

PDB; 21GG7; 09-AMG-01.

PDB; 21GG7; 09-AMG-01.

PDB; 21GG7; 09-AMG-01.

PDB; 21GG7; 01-MAN-04.

INTERPRO; 1PR001899; GTam pos anchor.

INTERPRO; 1PR000189; GTam pos anchor.

INTERPRO; 1PR000724; 1gG_bind_B.

PFAm; PF01468; GA; 3.
                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 168:319-324(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00746; Gram pos anchor; 1.
Pfam; PF01378; IgG_binding_B; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-G148;
MEDLINE-98290449; PubMed-9628485;
                                                                                                                                                                                                                         STRAIN=G148;
MEDLINE=88029445; PubMed=3665928;
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SEQUENCE OF 114-593 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 371-427.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=1320;
                                                                                                                                                                                                                                                                                                            streptococcal
                                                                                                                                                       Streptococcus
STRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variant
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us-09-455-978b-77.rsp

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KINL LEICH
P46865;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINL_LEICH
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                              98 AAAADALAKAKADALKEFNKYGVSDYYKNL-----INNAKTVEGVKDLQAQVV-- 145
                                                                                                                                                                                                                                                                                                                                                                                                       103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                            --GLSDFLKSQTPA---EDTVK 175
                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                TPIIRNGGE---LINLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAAAWEA
                                                                                                                                                                                                                                                                                                                                                                    ----QPLFEATADAL-----VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG
     PRINTS, PRO0015, GPOSANCHOR.
TIGRFAMS, TIGR01167, LPXTG anchor; 1.
TIGRPAMS, TIGR01167, LPXTG anchor; 1.
TIGRPAMS, TIGR01168, YSIRK_Signal; 1.
PROSITE, PS50847, GRAM POS ANCHORING; 1.
IgG-binding protein; Cell wall; Peptidoglycan-anchor; Repeat; Signal;
                                                                                                                                                                   5 X 5 AA REPEATS OF [DE]-D-A-K-K.
LPXTG SORTING SIGNAL (POTENTIAL).
AMIDE-LINKED TO CELL WALL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ACH0158 / Biovar 2;
STRAIN=ACH0158 / Biovar 2;
Jeong E.-L., Timmis J.N.;
"Putative lpxC gene from Ralstonia solanacearum ACH0158 strain.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                         IMMUNOGLOBULIN G BINDING PROTEIN G. REMOVED BY SORTASE (POTENTIAL).
                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                                                  ----DTMAALAAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UDP-3-O-[3-hydroxymyristoy1] N-acety1glucosamine deacetylase
(EC 3.5.1.-) (UDP-3-O-acyl-GlCNAc deacetylase).
                                                                                                                                                                                                                                                                                           DB 1; Length 593;
1.4;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                         63291 MW; 048BAA760D5B2920 CRC64;
                                                                                            ALA-RICH.
3 X 37 AA REPEATS
                                                                                                                                          X 55 AA REPEATS
                                                                                                                                                                                                                                                                                                                                10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 AA
                                                                                                                                                                                                                                                                                          Score 98; DB; Pred. No. 1.4; 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          -----ESAKKARISEATD-
PF04650; YSIRK_signal; 1.
                                                                                                                                                                                                                                                                                           10.5%;
25.3%;
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            163 AVDELVARFL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIELAEAKVĽ 185
                                                                                                                              290
427
357
427
555
563
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                                                                                                                                                                                                         386
                                                                                                                                                                                                                                                                         593 AA;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=305;
                                                      3D-structure
                                                                                                                                                                                                                                                                                                              48;
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                                                                                                                                                                                                                                                                         SEQUENCE
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STRAND
                                                                                                  DOMAIN
REPEAT
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REPEAT
DOMAIN
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STRAND
HELIX
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REPEAT
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                                                                         CHAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 YAAQRARIGKIHDVLGLGPDVY-----LGAYTRYYTG-----LLDALADD-----VV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IEFRHPAVDKTGQTFEIDFADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 DVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTDFYDH
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                                                 Salanoubat M., Genin S., Artignenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Remard C., Cunnes S., Demange N., Saspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Schiex T., Heissenback J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                        -!- FUNCTION: Involved in the biosynthesis of lipid A, a phosphorylated glycolipid that anchors the lipopolysaccharide the outer membrane of the cell (By similarity).
-!- CATALYTIC ACTIVITY: UDP-3-0-(3-hydroxytetradecanoyl)-N-acetylglucosamine + H(2)0 = UDP-3-0-(3-hydroxytetradecanoyl)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N -> T (IN REF. 1).

I -> T (IN REF. 1).

S -> A (IN REF. 1).

S -> A (IN REF. 1).

M. F531BBE1349FBBAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%; Score 90.5; DB 1;
24.6%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                             glucosamine + acetate.
-!- PATHWAY: Lipid A biosynthesis; second step.
-!- SIMILARITY: Belongs to the lpxC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 LESYERTQDLFANSTKTVEQLKETQAEYLLGLGRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 EVRDG-----DKLARLEPYFGFKLSFT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF254622; AAF75724.1; -.
EMBL; AL646072; CAD16544.1; -.
HAMAP: MF 00388; -; 1.
InterPro; IPR004463; LpxC.
Pfam; PF0331; LpxC; 1.
IIGRPAMs; TIGR00325; lpxC; 1.
Hydrolase; Lipid A biosynthesis; Lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 ADRGEEAAAVDELVARFLPMLK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----FLPQLQ 301
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STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33399 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Conservative
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132
155
279
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132
155
279
305 AA;
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TIG MYCLE
Q9CBY2;
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TIG MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 DDTMAALAAEQPLFEATADALVT---DFYDHLESYERTQDLFANSTKTVEQLKETQAEYL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 ESTVAQLEREQREREVALDALQTHQRKLQBALESSERTA---AERDQLLQQLTELQSE-R 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602 TQLSQVVTDRERLTRDLQRIQYEYGETELARDVALCAAQEMEARYHAAVFHLQTLLELAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X 39 AA APPROXIMATE TANDEM REPEATS
                                                                                                   Burns J.M. Jr., Shreffler W.G., Benson D.R., Ghalib H.W., Badaro
                                                                                                                                           "Molecular characterization of a kinesin-related antigen of Leishmania chagas; that detects specific antibody in African and American visceral leishmaniasis.";
Proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
-!- DEVELOPMENTAL STAGE: PREDOMINANT IN AMASTIGOTES.
-!- SIMILARITY: Belongs to the kinesin-like protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 LGLGRGEYDTE-YAAQRARIGKIHDVLGLGPDVYLGA----YTRYYTGLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINIS; PROCESS, 1.

SMART; SMOOLSE; 1.

PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

MOTOR protein; Microtubule; ATP-binding; Coiled coil; Repeat.

DOMAIN 1 399 KINESIN-MOTOR (BY SIMILARITY).

COLLED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 ---DALADDVVADRGEBAAAVDELV----ARFLPMLKLLTFDQQI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Glycerol-3-phosphate acyltransferase (EC 2.3.1.15) (GPAT).
PLSB OR ML1246 OR MLCB1610.07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ore 89; DB 1; Length 955 ed. No. 12; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       955 955
955 AA; 106168 MW; 8CA76815BE84C6E9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5%; Score 89; 29.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A47334; A47334.
HSSP; P17119; 3KAR.
INTECPED; IPPR010755; kinesin_motor.
Pfam; PF00225; kinesin_t.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                            STRAIN=MHOM/BR/82 / Isolate BA-2;
MEDLINE=93133867; PubMed=8421715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L07879; AAA29254.1; -.
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>955
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129
>955
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820
859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                    SEQUENCE FROM N.A.
NCBI_TaxID=44271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYCLE
                                                                                                                       Reed S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
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DOMAIN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SVSTLLF 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIAWRLSF----TGIDDDTMAALAABQPLFEATADALVTDFYDHLESYERTQDLFANSTK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: Acyl-CoA + sn-glycerol 3-phosphate = CoA + 1-acyl-sn-glycerol 3-phosphate.
-!- PATHWAY: De novo phospholipid biosynthesis; first step. May also function in the regulation of membrane biogenesis.
-!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
-!- SIMILARITY: Belongs to the GPAT / DAPAT family.
                                                                                                                                                                                  MEDLINE=21128732; PubMed=11234002;
Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00563; PisC; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        685 DVGQKELT--ELALGVGR-----OYVAQGRVRSGE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      775 AA; 87363 MW; 03DD77C778293CDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
TIGGOR ML1481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.4%; Scoll No. 12, 29.4%; Pred. No. 12, ina 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF 00393; -; 1.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL549913; CAB43153.1; -. EMBL; AL583921; CAC31627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 ALADDVVADRGEEAAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 ATAYQVVVDQNLIAPA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; T45238; T45238.
Leproma; ML1246; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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SEQUENCE 775 AA;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=1769;
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Wed Aug 11 13:19:17 2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSIDLSATINGEKVPNADAEGLSH-EVGYGRLIAGLDDALVGLSAGESRVF---TTQLAT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the FKBP-type PPIase family. Tig subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R HAMAP, MF. U0303; -; ..

R InterPro; IPR001179; FKBP_PPIase.
R InterPro; IPR006818; Trigger C.
R InterPro; IPR008881; Trigger C.
R InterPro; IPR008881; Trigger C.
R Pfam; PF00554; FKBP; 1.
R Pfam; PF00569; Trigger C; 1.
R Pfam; PF05699; Trigger C; 1.
DR PROSITE; PS00453; FKBP_PPIASE 1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE 2; PALSE_NEG.
DR PROSITE; PS000454; FKBP_PPIASE 2; PALSE_NEG.
DR PROSITE; PS00059; FKBP_PPIASE 2; PALSE_NEG.
DR PROSITE; PS00059; FKBP_PPIASE 2; PALSE_NEG.
DR PROSITE; PS00059; PKBP_PPIASE 2; PALSE_NEG.
                                                                                                                                                                                                                                                             -!- FUNCTION: Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation
                                                                                       Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Erown D., Chillingworth T., Connor R., Davies R.M., Davlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherfer S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 VTADVRNGIDGHAL--ADRIGLDEAEIAWRLSFTGIDDDTWAALAAEQPLFEATADALVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SKHAGOD--AEVIVTVKSVKERELPEPDDEFAQLVSEFDTMAELRANLGDQVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Indels 82; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAKYAQQAEKIRDAAVDALLERVDVPLPEGIVQAQFNNALHDALSGLGHD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGLLDALADDVVADRGE-----EAAAAVDELVARFLPMLKLLTFDQQI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45095F5BD231B884 CRC64;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 DFYDHLESYERTQDLFANSTKTVEQLKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.3%; Score 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š.
                                                                          MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL583922; CAC30431.1; -. PIR; B87094; B87094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 DTEYAAQRARI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 00303; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leproma; ML1481; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                 (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322
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957 AA.

PRT;

STANDARD;

SECA_MYCSM ID SECA_MYCSM

RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 HNVLNAKY------GNVDFL 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 YKTEEAKFLAVVDDVAERHAKGOPVLIGTT-----SVERSEYLSKMLTKRRVP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 LKETQAEYLLGLGRGEYDTEYAAQRARIGKI---HDVLGLGPDVYLGAYTRYYTGLLDAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                   35 WR---LSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQ
                                                                                                                                                                                                                                                                                                                              Brown A.B., Jacobs W.R.; "Conservation of the general secretory pathway: isolation and characterization of SecA homologues from Mycobacterium bovis BCG and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01312; SECA; 1.
Protein transport; ATP-binding; Membrane; Translocation; Transport. NP BIND 98 105 ATP (POTENTIAL).
SEQUENCE 957 AA; 107001 MW; AD208569A22BA32E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic side of membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 DNDTLVTADVRN-----GIDGHALAD-----RIGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70; Indels
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 ADDVVADRGEEAAAAVDELVARF---LPMLK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
-!- SIMILARITY: Belongs to the secA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.2%; Score 85.5; D
Best Local Similarity 21.8%; Pred. No. 24;
Matches 46; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || : :|| : || : || 5
505 ADKRLRERGLDPVETPEEYEAAWHEVLPQVK
                                                                                          Preprotein translocase secA subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR001650; Helicase C.
InterPro, IPR000185; SecA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00271; helicase C; 1.
Pfam; PF01043; SecA protein; 1.
PRINTS; PR00906; SECA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR00963; secA; 1.
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                                                                                                                                                      Mycobacterium smegmatis.
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q02228;
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Query Match
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                                                                                                                  NCBI_TaxID=12027;
                                             Bacteriophage SP
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                                                                                           Allolevivirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 HLESYERTQDLFANSTKTVEQLKETQAEYLLGLGR-GEYDTEYAAQRARIGKIHDVLGLG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                   STRAIN=DSM 1411;
MEDLINE=30201102; PubMed=1404376;
MEDLINE=30201102; PubMed=1404376;
Englert C., Krueger K., Offner S., Pfeifer F.;
Three different but related gene clusters encoding gas vesicles in halophilic archaea.";
J. Mol. Biol. 227:586-592(1992).
-!- FUNCTION: May confer stability to the gas vesicle membranes. Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the positioning of the organism at the favorable depth for growth.
-!- SUBCELLULAR LOCATION: Binds to the external surface of the gas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 RDGHKDVADAFLQYREFHGVEVQSLLDNIAAFQREMGDYRKAFETTEEAFASF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 PDVY----EAAYTRY---YTGL-LDALADDVVADRGE-----EAAAAVDELVARF 171
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; 9FB48199D0305921 CRC64;
                                                                                                                       Halobacterium mediterranei (Haloferax mediterranei).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
228-FEB-2003 (Rel. 41, Last annotation update)
Gas vesicle protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S28115; S28115.
InterPro; IPR008639; Halo_GVPC.
Pfam; PF05465; Halo_GVPC; 1.
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                                                                                                                                                                        Halobacteriaceae; Haloferax.
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Best Local Similarity 25.2.
Local 45; Conservative
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59
122
160
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vesicle membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gas vesicle; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYANOBACTERIA.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=2252;
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VA1_BPSP
ID VA1_B1
AC P0967
DT 01-MA1
DT 01-MA1
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01_MAR 1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update)

STANDARD;

VA1 BPSP P09677;

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MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Alckey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Weetbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M.,
                                                                                Viruses; saRNA positive-strand viruses, no DNA stage; Leviviridae;
                                                                                                                                                                                                                                                    Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.; "Analysis of the complete nucleotide sequence of the group IV RNA
                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Not yet known.
-!- MISCELLANEOUS: The readthrough protein Al includes the coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 LSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last annotation update)
Glutamate 5-kinase (BC 2.7.2.11) (Gamma-glutamyl kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     READTHROUGH PROTEIN A1.
4A6642E4B52C6582 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 DALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ERGDEVSVTFDYALEDFLGNTNWRNWDORL
15-MAR-2004 (Rel. 43, Last annotation update) Readthrough protein Al [Contains: Coat protein]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.8%; Score 82; DB 1;
24.5%; Pred. No. 14;
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                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=88289362; PubMed=3399390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S01964; S01964.
HSSP; P03615; 10BE.
InterPro; IPR002703; Levi_coat.
Pfam; PF01819; Levi_coat; 1.
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16-OCT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 AA; 36203 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X07489; CAB37299.1; -.
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576 VVAADDGVQPQTKEAISHAKAAGVPLIVA 604
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552
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 VILTDRDGMFDADPRNNPDAQLIYEARADDPQLDAVAGGSAGALGRGGMQTKLRAARLAA 229
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                                                                                                                                                                 glutamate
5-
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                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP + L-glutamate = ADP + L-glutamate 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
                                                                                                                                                     FUNCTION: Catalyzes the transfer of a phosphate group to to form glutamate 5-phosphate which rapidly cyclizes to 5
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Kinase; Proline biosynthesis; Complete proteome.
DOMAIN 280 358 PHA.
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25.3%; Pred. No. 16;
Ive 19; Mismatches 66; Indels
                                                                                                                                                                                                                                                                       SEQUENCE 372 AA; 39845 MW; FAF2E81F6A8DEC36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Translation initiation factor IF-2.
INFB OR SLR074.
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 RIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVA-
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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PROSITE; PS00902; GLUTAMATE_5_KINASE; 1.
PROSITE; PS50890; PUA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004870; AAG07953.1; -.
PIR; G83074; G83074.
HAMAP; MF 00456; -; 1
InterPro; IPR001048; Aa kinase.
InterPro; IPR001057; Glu 5kinase.
InterPro; IPR00157; Glu 5kinase.
InterPro; IPR00157; Glu 5kinase.
InterPro; IPR002479; Pub.
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Pfam; PF01472; PUA; 1.
PRINTS; PR00474; GLUSKINASE.
SMART; SM00359; PUA; 1.
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                                                                                               opportunistic pathogen.";
Nature 406:959-964(2000).
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MEDLINE-97061201; PubMed=8905231;
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MEDLINE-97061201; PubMed=8905231;
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MAYAJIMA N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
MARCHAIN S., Shimpo S., Takeuchi C., Mada T., Matanabe A.,
Yamada M., Yasuda M., Tabeta S.,
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or send an email to license@isb-sib.ch).
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INTERPRO! _IPRO00795; EF GTPbind.

INTERPO: IPRO00795; EF GTPbind.

INTERPO: IPRO00718; IF2.

INTERPO: IPRO008225; SMAIL GTP.

INTERPO: IPRO008225; SMAIL GTP.

INTERPO: IPRO008225; SMAIL GTP.

INTERPO: IPRO00900; Translat_factor.

Pfam; PF03144; GTP EFTU; I.

Pfam; PF04760; IF2 N; 2.

Pfam; PF04760; IF2 N; 2.

PRINTS; PR00315; BIONGANNET.
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TIGRFAMS; TIGR00231; small GTP; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                Hou S., Brooun A., Yu H.S., Freitas T., Alam M.;

"Sensory thodopsin II transducer Hirli is also responsible for serine chemotaxis in the archaeon Halobacterium salinarum.";

"Bacteriol. 180:1600-1602(1998).

-!- FUNCTION: Transduces signals from the phototaxis receptor sensory rhodopsin II (SR-II) to the flagellar motor. Responds to light changes through the variation of the level of methylation. Also acts as a chemotransducer.

-!- SUMSCELEULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Contains 1 methyl-accepting transducer domain.
                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis
protein II) (MPP-II).
                                                                                                                                                                                                                                        MEDLINE=96323203; PubMed=8710852;
Zhang W., Brooun A., Mueller M.M., Alam M.;
"The primary structures of the Archaeon Halobacterium salinarium blue
light receptor sensory rhodopsin II and its transducer, a methyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transducer; Photoreceptor; Chemotaxis; Transmembrane; Methylation;
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                                                                                                                           Halobacterium salinarium.
Archaea, Euryarchaeota, Halobacteria, Halobacteriales;
Halobacteriaceae, Halobacterium.
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                         accepting protein.";
Proc. Natl. Acad. Sci. U.S.A. 93:8230-8235(1996)
 764 AA
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InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
 PRT;
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Pfam; PF00015; MCPsignal; 1.
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SMART; SM00283; MA; 1.
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469
764 AA;
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8.6%; Score 80.5; DB 1; Length 764;

Query Match

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                                                                        552 DDAEAAADAMDALDSEMADIGEIVDVIADIADQTNMLALNASIEAARTGADGDGFAVVAD 611
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               61; Gaps
               77; Indels
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21.4%; Pred. No. 47; tive 31; Mismatches
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Best Local Similarity
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Search completed: August 10, 2004, 15:26:51 Job time : 6.79177 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 10, 2004, 15:22:05; Search time 22.0533 Seconds (without alignments) 2632.505 Million cell updates/sec

US-09-455-978B-77 933

1 MSNDNDTLVTADVRNGIDGH.........DELVARFLPMLKLLTFDQQI 184 Title: Perfect score: Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archea:*

3: sp_bacteria:*

4: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

sp_unclassified:* sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_organelle:*sp_phage:* sp_rodent:* sp_plant:* virus:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp archeap:

SUMMARIES

•			Description		O9kfh4 bacillus ha	Ogabo Gan Orace	OSual O agrobacteri	Ogasyon can observe	OB14k6 hadiling de	OBd4h1 vibrio muln	OBs4w2 rigits vitin	Copper prize to the control of the copper control of the copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper copper c	Coops acrepromyce	Q84gk0 escherichia	OBITHO Dacillus an	OBW607 hacterionha	Oghrw3 halobacteri	ORSWING STREET OWNER	OKA476 Personal Control	Office draptachangers	Normy Dincerra an	Q8ujal agrobacteri
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	439 AA.		ence	01-OCT-2003 (TrEMBLrel, 25, Last annotation undate)				Bacteria; Firmicutes; Bacillales; Bacillaceae: Bacillus						Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masni N	Fuji F., Hirama C., Nakamura Y., Oqasawara N., Kuhara S		"Complete genome sequence of the alkaliphilic bacterium Bacillus	halodurans and genomic sequence comparison with Bacillus subtilis.
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illus otilis.";

Nucleic Acids Res. 28:4317-4331(2000).

EMBL; AP001508; BAB04224.1;

EMBL; AP001508; BAB04224.1;

EPTR; AB3713; AB3713.

GO: GO:0016020; C:membrane; IEA.

GO: GO:0004871; F:sugar porter activity; IEA.

GO: GO:0005351; F:sugar porter activity; IEA.

GO: GO:0005351; F:sugar porter activity; IEA.

GO: GO:0004811; F:sugar porter activity; IEA.

GO: GO:0004801; F:sugar porter activity; IEA.

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GO: GO:000401; F:sugar porter activity; IEA. RA RA RA RA RA RA RA DR DR DR DR DR DR DR DR SQ SQ SQ

PROSITE; PS50111; CHEMOTAXIS TRANSDUC_2; 1.
PROSITE; PS00589; PTS_HPR_SER; 1.
Complete protecome.
SEQUENCE 439 Aa; 48918 MW; 1E092BB2F42592AE CRC64;

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SEQUENCE FROM N.A.

MEDLINE=1608551; PubMed=11743194;
A Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
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R EMBL; ABC09067; AAL42040.1; -
R EMBL; ABC09067; AAL42040.1; -
R EMBL; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC093067; AAL42040.1; -
R PIRB; ABC008037; AAR6834.1; -
71 SRQQAHWGV-IAEGQFSDDYVQAVRAIGQTHARIGLEPRWYIGGYAVVGDHLVRAVIDSM 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-Z1608550; PubMed=11743193; Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bowee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Ii M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester B.W.;
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01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-UNN-2003 (TrEMBLrel. 21, Last annotation update)
Methyl-accepting chemotaxis protein.
MCPV OR ATU1027 OR AGR_C 1888.
Bacrberium tumefaciens (strain CS8 / ATCC 33970).
Bacreria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiane/Agrobacterium group; Agrobacterium.
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GO; GO: 0004871; F: signal transducer activity; IEA.
GO; GO: 0004871; F: signal transducer activity; IEA.
GO; GO: 0005815; P: chemoctaxis; IEA.
InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR004689; Chmtaxis transd.
InterPro; IPR004680; Me Chemotaxis.
Pfan; PF00015; MCP8ignal; 1.
PRINTS; PR00260; CHEMTRNSDUCR.
                                                                      ----VADRGEEAAAVDELVARFLPM 174
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PROSITE; PS50885; HAMP; 1.
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SMART; SM00283; MA; 1.
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SEQUENCE 499 AA;
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MEDLINE=21173699; PubMed=11259647;

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MEDLI, MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY S.L., MEDLORSY
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                                                                                                                                                                                                                                                                        EQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALA 149
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                                                                                10; Gaps
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                    Length 439;
                                                                             Indels
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GO: GO: 0004871; F: signal transducer activity; IEA.
GO: GO: 0006915; P: chemotaxis; IEA.
GO: GO: 00007165; P: signal transduction; IEA.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
InterPro; IPR003660; HAMP.
FO: FO: IPR0036090; Me Chemotaxis.
PF00015; MCP8ignal; 1.
             15.9%; Score 148; DB 16; I
25.2%; Pred. No. 0.00015;
ive 35; Mismatches 71;
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             Query Match
Best Local Similarity 25.2
Matches 39; Conservative
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SMART; SM00283; MA; 1.
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SEQUENCE 537 AA;
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STRAIN=ATCC 19089 / CE15;
MEDLINE=21173698; PubMed=11259647;
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"Complete genome sequence of Caulobacter creecentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 AEIAWRLSFTGIDDDTWAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 105.5; DB 16; Length 555; 24.7%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            555 AA; 59114 MW; C9560265C1EC0B31 CRC64;
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PRE, D87536; D87536.
HSSP, P02942; LQU7.
TIGR; CC2317; -. GO:0016020; C:membrane; IEA.
GO: GO:0016871; F:signal transducer activity; IEA.
GO: GO:0006935; P:chemocaxis; IEA.
GO: GO:0004871; P:chemocaxis; IEA.
GO: GO:0006935; P:signal transduction; IEA.
InterPro: IPR004089; Chmtaxis_transd.
InterPro: IPR003660; HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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PROSITE; PS50885; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence
01-JUN-2003 (TrEMBLrel. 24, Last annotati
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
                                                                                                                                                                          139 RYYTGLLDALAD 150
                                                                                                                                                                                                         |::|::
116 LMLDGIVKAVIE 127
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                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC2317.
Caulobacter crescentus
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Matches 40: Consorm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=155892;
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SEQUENCE 555 AA;
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                                                                                                                                                                                                                                                                                               RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 -----TVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 AEIAWRLSFTGIDDDTWAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTK---
                                                                                                                                                                                                                                                                           MEDINE=22608415; PubMed=12721630; Ivanova N., Candelon B., Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Overbbeek R., Kyrpides N.; Overbbeek R., Kyrpides N.; Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.9%; Score 102; DB 16; Length 434; 20.5%; Pred. No. 1.7; ive 27; Mismatches 71; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 RYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 ELFRSIIKILQTKI------TTIDDFSYSINVINKLFTLEGEL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71; Indels
                                                                                                                                                           Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Vibrio vulnificus CMCP6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 AA; 49441 MW; B1007BA0230620C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 423:87-91(2003).

EMBL; AE017015; AAP12286.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004971; F:signal transducer activity; IEA.
GO; GO:0006395; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004089; Cimtaxis transd.
InterPro; IPR004089; Cimtaxis transd.
InterPro; IPR004099; Me chemotaxis.
Pfam; PP00015; MCPsignal, 1.
PRINTS; PR00260; CHEMTRNSDUCR.
                                                                           Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
       434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00283; Ma; 1.
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
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                                                   Created)
                                                                                                                  Methyl-accepting chemotaxis protein.
    PRT;
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                                         01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Conservative
  PRELIMINARY;
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Matches 34; Conserv
                                                                                                                                                                                                       NCBI_TaxID=226900;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE 434 AA.
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Q814K6
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64 LV-TDFYDHLESYERTQDLFANSTKTVEQ-----LKETQAEYLLGLGRGEYDTEYAAQ 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 RARIGKIHD---VLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 TLVTADVRNGIDGHALADRIGLDEAEI--AWRLS-FTGIDDDTWAALAAEQPLFEATADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2) / M145,
MBDLINE=21996410; PubMed=12000953;
MBDLINE=21996410; PubMed=12000953;
MBDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitesh E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Watren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147\{2002\}.
                                                                                                                                                                                                       Streptomyces coelicolor.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77; Indels
                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                           B.G., Rajandream M.A.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D22747AF816D1DE4 CRC64;
                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                     218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome. SEQUENCE 218 AA; 23670 MW; D22747AFF
                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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                                                                                                                 01-NOV-1998 (TYEMBLEGL. 08, C
01-NOV-1998 (TYEMBLEGL. 08, L
01-OCT-2003 (TYEMBLEGL. 25, L
HYPOCHECICAL PYCCEIN SCOG675.
SCOG675 OR SC5A7.25C.
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SMART; SM00530; HTH XRE; 1.
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Submitted (JUL-1998)
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217 SKLLK 221
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Parkhill J., P
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                                                                                       088031
                                                     RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETIVMVEANRAKFEH-----IDAAEIASRKAFVAATRKELQAVSTEISTDTVKTRIRK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 EERKIMQPAKSS--TSFRSNLTGQERNERFLEDETOROOGIMOEONDSLAGL----- 170
                                                                                                                                                                                                                                   663
                                                                                                                                                                                                                                                                                            724 ANVEGHQYTVENLYDDIWMGYSYTQWFDRNIDLIAE---VDRLLEQGVPVDQITPEMIPN 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                      ---YLLGLGRGEYDT-----EYAAQ 115
                                                                                                                                                                                                                                                                                                                                           116 RARIGKIHDVLGLGPDVYLG-AYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPM 174
                                                                                                                                                                                                 ----ERTODLFANSTKTV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TGIDDDTMAA--LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 AEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDINE=21947832; MEDINE=21947832; PubMed=11950882; Dacks J.B., Dolittle W.F.; "Novel syntaxin gene sequences from Giardia, Trypanosoma and algae: "Novel syntaxin gene sequences from Giardia, Trypanosoma and algae: implications for the ancient evolution of the eukaryotic endomembrane
                                                                                                                                                                                                                                   606 DSENTYRLTEHOPIWSSPTDSSYEEYADY--NYNNOKWENRTAYWVERTTELLADSSTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                              53;
                                                                                                                              Length 1222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytophthora infestans (Potato late blight fungus).
Bukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                              Indels
                                                                                           B04525D301FA99E2 CRC64;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2FE6891BA5AA0067 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5%; Score 97.5; DB 10; 22.7%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          £13
                                                                                                                              DB 16;
                                                                                                                                                                                                 43 DDDTMAALAAEQPLFEATADALVTDFYDHLESY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 DTLVTADVRNGIDGHALADRIGLDEAEIAWRLSF----
                                                                                                                 10.6%; Scc...
20.2%; Pred. No. 1...
14e 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Mismatches
   Submitted (DEC-2002) to the EMBL/GenBank, EMBL, AE016813; AA008278.1; -
InterPro; IPR000437; Prok lipoprot S. PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Hypothetical protein; Complete proteome. SEQUENCE 1222 AA; 136974 MW; B04525D
                                                                                                                                                                                                                                                                          ------EQLKETQAE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Cell Sci. 115:1635-1642 (2002).

EMBL; AP404749; AAM12665.1; -.

InterPro; 1PR000727; T. SNARE.

Pfam; PF05739; SNARE; I.

SMART; SM00397; t. SNARE; 1.

PROSITE; PS50192; T. SNARE; 1.

PSCOITE; PS50192; T. SNARE; 1.
                                                                                                                         Query Match
Best Local Similarity 20.2*
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 LPMLK 176
                                                                                                                                                                                                                                                                                                                                                                                                                   175 LKL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                       781 LNL 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytophthora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
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Matches
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28;

Length 218;

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Bacteriophage phiE125.
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                                                                                                                                                                                                                                                                                          Fraser C.M.;
                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8W6U7;
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READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX READ OX RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1012 NVTLITAP--KGSDENTFKAGTQQIGF--SNİTPEIRTENTDTATQWVLTGYQSVADARA 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DALVIDFYDHLESYERTQDLFANSTKTVEQLKETQ-----AEYLLGLGRGE--YDTEYA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AQRARIGKIHDVLGLGPDVYLGAYTRY-----YTGLLDALADDVVADRGEEAAAAV 164
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 NDTLVTADVRNGIDGH---ALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                  83; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1364 AA; 147696 MW; 33B341FDAB6859E2 CRC64;
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Bacillus anthracis (strain Ames).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                        A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   Fleckenstein J.M., Patel S.K., Dotson J.,
                                                                                                                      PRT; 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGR01414; autotrans_barl; 1.
                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methyl-accepting chemotaxis protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03797; Autotransporter; 1.
Pfam; PF02395; IGA1; 1.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00921; IGASERPTASE
                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Conservative
                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |: ::|
1184 D-LIGKYL 1190
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                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=H10407;
                                                                                                                                                                                                                                                                                Plasmid pcs1
                                                                                                                                                         01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                       Q84GK0;
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                                                                                                                  Q84GK0
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ID Q8
DT Q8
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DT 01
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80 LITIIERYSSIPKLKQTLKTHIKELFSGDMHEDFIEQRVKIAKRHVQIGLHRKWYTAAYQ 139
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               Read T.D., Peterson S.N., Tourasse, N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Nelson Holtzapaple B.K., Okstead O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.E., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 AEIAWRLSFTGIDDDIMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 -----TVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Woods D.E., Jeddeloh J.A., Fritz D.F., DeShazer D.;
"Burkholderia thailandensis El25 Harbors a Temperate Bacteriophage
                                                                                                                                                                                                                                                                                       "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 RYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Specific for Burkholderia mallei.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF447491; AAL40277.1;
InterPro; IPR006944; Phage portal.
InterPro; IPR006427; Portal HK97.
Pfam; PF04860; Phage portal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 AA; 49391 MW; E06512BA0E696D92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016020; C:membrane; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0006335; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR004090; Me chemotaxis.
PF00015; MCP8ignal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 SELKVQMDMLHISKEDLQIVKVLQPFIYEEIDWITEKFY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.2%; Score 95; DB 16;
19.3%; Pred. No. 6.9;
tive 29; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00283; MA; 1.
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419
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MEDLINE=22608414; PubMed=12721629;
                                                                                                                                                                                                                                                                                                                                     Nature 423:81-86(2003).
EMBL; AE017041; AAP29306.1; -.
TIGR; BAS673; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00260; CHEMTRNSDUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.2%
Best Local Similarity 19.3%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses, dsDNA viruses,
Lambda-like viruses.
NCBI_TaxID=180504;
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82 İR-İKPNRRRYTQQEIADGAGMSRQQAGALIN-GDRRPTMEHCDAIQRFFRVHAGFLTAE 139
----DAADVLERYEESRTALADVEETIADVREAVAE-----AERERETLADRVSDHRE 286
                                                                                                                                                                                                                    78 TODLFANSTKTVEQ-----LXETQAEYLLGLGRGEYDTEYAAQRARIGKIHD--VLGL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 ALADRLGVAHAEVFDVGRLSVASGVPEPVVKALLSGRPAGEPDLQA---RFLQRLDLIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ALADRIGLDEAEI--AWRLSF-TGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYER
                                                                                                                                                                                        118 RIGKIHDV-----LGL-GPDVYLGAYTRYYTGLLDALAD--DVVADRGEEAAAAVDEL
                                                                                63 ALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINEMA 4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=2147403; PubMed=11572946;
OMUTA S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M., Genome sequence Of an industrial microorganism Streptomyces avermitiils: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.1%; Score 94; DB 16; Length 218; 28.7%; Pred. No. 3.1; tive 22; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 GPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 AA; 24060 MW; 3277B89A840B4C73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL, AP005028: BAC65453.1;
GO, GO.0003677; F.DNA binding; IEA.
InterPro; IPR001387; HTH 3.
Fram; PF01381; HTH 3.
SMART: SMO0530; HTH XRE; I.
Complete proteome.
SRQUENCE 218 AA; 24060 MW; 3277B89A840B4
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                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Matches 47; Conserv
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01-OCT-2003
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064476
ID 06447
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                                                                                                                                                 10;
                                                                                                                                                                                                                                          201 NGTALSGVIERPKDAPALKDQASVDRITDGWNAKFGGSGNAKKVALLQEGMTFRPLSMTN 260
                                                                                                                                                                                                                                                                                                                                                         261 VDAALIDALRLSALDIARIYKIPAHWVNELERATFSNIEHQSLOFVIYTLLPWVKRHEQA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                             321 KTRDLLLPSER-----KQYFIEYNLAGLLRGDQSSRYAAY--AVGRQWGMLSINDIRRLE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005224; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003439; ABC transporter.
InterPro; IPR003405; SMC_N.
InterPro; IPR003405; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDZINE=20504483; PubMed=11016950; NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Welt H.D., Lasky S.R., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.B., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
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                                                                                                                                                                                                5 NDTLVTADVRNGIDGHALADRIGLDBAEIAWRLSFTGIDDDTMAALAAE----QPLFEAT
                                                                                                                                                                                                                                                                                                                                                                                                              RIQDLFANSTKTVEQLKETQAEY-LLGLGRGEYDTEYAAQRARIGK-----IHDVLGL-
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                                                                                      10.1%; Score 94.5; DB 9; Length 419; 21.7%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 -----GPDVYLGAYTRYYTGLLDA-LADDVVADRGEEAAAAVDEL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 NMPPVKGGDIYLSP-----MNMVDASKPQQLPVGKSEPTKAAIDEI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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             TIGRFAMS; TIGR01537; portal HK97; 1. SEQUENCE 419 AA; 46404 MW; C15C3CC08F21D2C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Score 94.5; DB 17; 28.3%; Pred. No. 21; ative 23; Mismatches 63;
                                                                                                                                                                                                                                                                                                          ---FYDHLE-
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                                                                                                                  1 Similarity 21.7%; Pred. No. 7.2; 49; Conservative 28; Mismatches
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                                       46404 MW;
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01-MAR-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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SEQUENCE 883 AA;
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                                                                                              Query Match
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SEQUENCE FROM N.A.

MEDLINE=20083487; PubMed=10617197;

MEDLINE=20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 GRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALA------D
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MEDLINE=22247741; PubMed=12271122;
Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Peptide ABC transporter, periplasmic peptide-binding protein.
BRA1099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 94; DB 10; Length 1090;
; Pred. No. 31;
17; Mismatches 55; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1090 AA; 121522 MW; EB170342E18DCA1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002392; AAD12029.1; -.
PIR; T00533; T00533.
                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Putative DNA2-NAM7 helicase family protein.
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                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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26.9%;
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nes 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts."; Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

EMBL; ARO14601; AAN34255.1; -. GO; GO:000515; F:transporter activity; IEA.

GO; GO:000515; F:transporter activity; IEA.

GO:0000610; PROSONA; SBP Bac.5; 2.

FROMITE: PSO1040; SBP Bac.5; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ADALVIDFYDHLESYERIQDLFANSTKIVEQLKETQABYLLGLGRGEYDTEY--AAQRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 IGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAA-----AAVDELVARF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 514;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 10.0%; Score 93.5; I Similarity 27.1%; Pred. No. 12; 49; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| |: || |: || 83 LSEDSKTL-TFKLRKGVKFH-
                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
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